

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:30:15 ; Search time 42.1791 Seconds
 (without alignments)
 120.578 Million cell updates/sec

Title: US-09-641-802-3
 Perfect score: 98
 Sequence: 1 DQPPDVEKPDLPFQVQS 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 422553

Minimum DB seq length: 7
 Maximum DB seq length: 18

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length	Length			
1	98	100.0	18	4	AAB72502	Aab72502	Colostrin
2	98	100.0	18	4	AAB59325	Aab59325	Ewe colos
3	98	100.0	18	4	AAB72248	Aab72248	Colostrin
4	98	100.0	18	4	AAB72534	Aab72534	Colostrin
5	98	100.0	18	5	AAO14579	Aaol4579	Neural ce
6	98	100.0	18	5	AAM51038	Aam51038	Colostrin
7	98	100.0	18	5	AAE20230	Aae20230	Colostrin
8	41	41.8	15	5	ABG67986	Abg67986	Human ADP
9	41	41.8	15	6	ADA24138	Ada24138	Alzheimer

10	39	39.8	16	2	AAR49858	Aar49858	Sequence
11	39	39.8	16	6	ABP83082	Abp83082	G protein
12	36	36.7	15	5	AAM47777	Aam47777	Short cha
13	35	35.7	12	5	ABG67771	Abg67771	Human ADP
14	35	35.7	12	6	ADA23910	Ada23910	Alzheimer
15	35	35.7	13	3	AAB26624	Aab26624	Partial s
16	34	34.7	13	5	ABB97740	Abb97740	Human pro
17	34	34.7	13	5	ABB97739	Abb97739	Human pro
18	33	33.7	15	3	AAB21134	Aab21134	Src homol
19	33	33.7	18	2	AAy41624	Aay41624	Mammalian
20	33	33.7	18	6	AAE34138	Aae34138	T-cell st
21	33	33.7	18	6	AAE34142	Aae34142	T-cell st
22	33	33.7	18	6	AAE34133	Aae34133	T-cell st
23	32	32.7	11	3	AAB21124	Aab21124	Src homol
24	32	32.7	11	3	AAB21133	Aab21133	Src homol
25	32	32.7	17	4	AAU01841	Aau01841	Wheat pep
26	32	32.7	17	4	AAU01840	Aau01840	Wheat pep
27	32	32.7	18	2	AAW38909	Aaw38909	Peptide r
28	31	31.6	10	4	AAG97089	Aag97089	Human com
29	31	31.6	11	2	AAW17451	Aaw17451	Consensus
30	31	31.6	11	5	ABP61522	Abp61522	Human KRP
31	31	31.6	15	2	AAW45819	Aaw45819	Peptide r
32	31	31.6	15	2	AAW45614	Aaw45614	Peptide r
33	31	31.6	16	2	AAW09376	Aaw09376	Proline-r
34	31	31.6	16	2	AAW09377	Aaw09377	Proline-r
35	31	31.6	17	2	AAW12220	Aaw12220	Human ace
36	31	31.6	18	2	AAW09378	Aaw09378	Proline-r
37	30.5	31.1	11	2	AAR44563	Aar44563	Encoded b
38	30	30.6	9	5	ABP55802	Abp55802	B15 class
39	30	30.6	9	5	ABG96846	Abg96846	Human leu
40	30	30.6	9	5	ABG96954	Abg96954	Human leu
41	30	30.6	9	5	ABG96698	Abg96698	Human leu
42	30	30.6	11	7	ADC35017	Adc35017	Rho-like
43	30	30.6	13	5	ABB97741	Abb97741	Human pro
44	30	30.6	15	4	AAG88540	Aag88540	HER2/NEU
45	30	30.6	15	6	ABR30154	Abr30154	Human can
46	30	30.6	15	7	ADE70385	Ade70385	Human 161
47	30	30.6	15	7	ADE70790	Ade70790	Human 161
48	30	30.6	15	7	ADE70192	Ade70192	Human 161
49	30	30.6	17	4	AAU01833	Aau01833	Wheat Gli
50	30	30.6	17	4	AAU01822	Aau01822	Wheat Gli
51	29.5	30.1	18	3	AAy79501	Aay79501	Eimeria t
52	29	29.6	8	5	AAU82343	Aau82343	Human pap
53	29	29.6	9	5	ABG69555	Abg69555	Human CRP
54	29	29.6	10	2	AAR10268	Aar10268	Human ven
55	29	29.6	10	4	AAG96833	Aag96833	Human com
56	29	29.6	10	6	ABU90826	Abu90826	Peptide #
57	29	29.6	10	7	ADE70033	Ade70033	Human 161
58	29	29.6	11	3	AAB21127	Aab21127	Src homol
59	29	29.6	13	5	ABJ01202	Abj01202	Human Sox
60	29	29.6	15	1	AAP50841	Aap50841	Sequence
61	29	29.6	15	1	AAP82092	Aap82092	HRV2-deri
62	29	29.6	15	3	AAy93323	Aay93323	Antigenic
63	29	29.6	15	6	ABR30262	Abr30262	Human can
64	29	29.6	15	6	ABR30229	Abr30229	Human can
65	29	29.6	15	7	ADB67139	Adb67139	Human rhi
66	29	29.6	15	7	ADC35688	Adc35688	Peptide e

67	29	29.6	17	6	ABP82697	Abp82697 G protein
68	29	29.6	18	4	AAG98704	Aag98704 Human cel
69	28	28.6	9	6	ABU75492	Abu75492 Novel pro
70	28	28.6	9	6	ABU72741	Abu72741 Novel pro
71	28	28.6	9	6	ABU76002	Abu76002 Novel pro
72	28	28.6	9	6	ABU74930	Abu74930 Novel pro
73	28	28.6	9	6	ABU76707	Abu76707 Novel pro
74	28	28.6	9	6	ABU73368	Abu73368 Novel pro
75	28	28.6	10	6	ABU77821	Abu77821 Novel pro
76	28	28.6	10	6	ABU73000	Abu73000 Novel pro
77	28	28.6	10	6	ABU74640	Abu74640 Novel pro
78	28	28.6	10	6	ABU73612	Abu73612 Novel pro
79	28	28.6	10	6	ABU75215	Abu75215 Novel pro
80	28	28.6	10	6	ABU74135	Abu74135 Novel pro
81	28	28.6	10	6	ABU77684	Abu77684 Novel pro
82	28	28.6	10	6	ABU76282	Abu76282 Novel pro
83	28	28.6	11	5	AAE18843	Aae18843 Human cal
84	28	28.6	12	2	AAW16014	Aaw16014 Peptide c
85	28	28.6	12	2	AAW16260	Aaw16260 Peptide c
86	28	28.6	12	2	AAW16004	Aaw16004 Peptide c
87	28	28.6	12	2	AAW68652	Aaw68652 Random pe
88	28	28.6	12	2	AAW68884	Aaw68884 Peptide b
89	28	28.6	12	2	AAW68643	Aaw68643 Random pe
90	28	28.6	12	2	AAW58122	Aaw58122 T6 interl
91	28	28.6	12	2	AAW58364	Aaw58364 Interleuk
92	28	28.6	12	2	AAW58131	Aaw58131 T6 interl
93	28	28.6	12	2	AAY09775	Aay09775 Interleuk
94	28	28.6	12	2	AAY09766	Aay09766 Interleuk
95	28	28.6	12	2	AAY10036	Aay10036 Interleuk
96	28	28.6	12	3	AAB17854	Aab17854 IL-1 anta
97	28	28.6	12	3	AAB17569	Aab17569 IL-1 anta
98	28	28.6	12	3	AAB17579	Aab17579 IL-1 anta
99	28	28.6	12	5	ABB72465	Abb72465 Interleuk
100	28	28.6	12	5	ABB72745	Abb72745 Interleuk

ALIGNMENTS

RESULT 1

AAB72502

ID AAB72502 standard; peptide; 18 AA.

XX

AC AAB72502;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #3.

XX

KW Dermatological; oxidative stress regulator; colostrinin.

XX

OS Unidentified.

XX

PN WO200112650-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022665.
 XX
 PR 17-AUG-1999; 99US-0149310P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2001-218342/22.
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the cell
 PT with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations.
 XX
 PS Claim 6; Page 25; 48pp; English.
 XX
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPFQVQS 18
 |||||
 Db 1 DQPPDVEKPDLPFQVQS 18

RESULT 2

AAB59325

ID AAB59325 standard; peptide; 18 AA.

XX

AC AAB59325;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment B-10.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
DR WPI; 2001-071058/08.
XX
PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.
XX
PS Claim 7; Page 27; 63pp; English.
XX
CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPPDVEKPDLPFQVQS 18
| | | | | | | | | | | | | | | |
Db 1 DQPPDVEKPDLPFQVQS 18

RESULT 3
AAB72248
ID AAB72248 standard; peptide; 18 AA.
XX
AC AAB72248;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 3.
XX
KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
PN WO200111937-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US022818.
XX

PR 17-AUG-1999; 99US-0149311P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2001-202804/20.
 XX
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator.
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides
 CC have immune response modulatory activity, and are capable of inducing
 CC cytokines. Colostrinin and its derived peptides are useful for inducing
 CC cytokine production, for modulating an immunological response and for
 CC inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPFFQVQS 18
 |||||
 Db 1 DQPPDVEKPDLPFFQVQS 18

RESULT 4

AAB72534

ID AAB72534 standard; peptide; 18 AA.

XX

AC AAB72534;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #3.

XX

KW Neuroprotective; neural cell differentiation regulator; colostrinin;

KW colostrum.

XX

OS Unidentified.

XX

PN WO200112651-A2.

XX

PD 22-FEB-2001.

XX
 PF 17-AUG-2000; 2000WO-US022774.
 XX
 PR 17-AUG-1999; 99US-0149633P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I;
 XX
 DR WPI; 2001-226545/23.
 XX
 PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating damaged
 PT neural cells in a patient.
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPPDVEKPDLPFFQVQS 18
 |||||
 Db 1 DQPPDVEKPDLPFFQVQS 18

RESULT 5
 AAO14579

ID AAO14579 standard; peptide; 18 AA.
 XX
 AC AAO14579;
 XX
 DT 27-MAY-2002 (first entry)
 XX
 DE Neural cell regulatory colostrinin peptide 3.
 XX
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 18
 FT /note= "Optional C-terminal amide"
 XX
 PN WO200213851-A1.
 XX
 PD 21-FEB-2002.
 XX

PF 17-AUG-2000; 2000WO-US022777.
 XX
 PR 17-AUG-2000; 2000WO-US022777.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I, Stanton JG, Hughes TK;
 XX
 DR WPI; 2002-269152/31.
 XX
 PT Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 7; Page 21; 37pp; English.
 XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPFQVQS 18
 |||||
 Db 1 DQPPDVEKPDLPFQVQS 18

RESULT 6

AAM51038

ID AAM51038 standard; peptide; 18 AA.

XX

AC AAM51038;

XX

DT 30-MAY-2002 (first entry)

XX

DE Colostrinin constituent peptide.

XX

KW Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 18

FT /note= "optional C-terminal amidation"

XX

PN WO200213849-A1.

XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022775.
XX
PR 17-AUG-2000; 2000WO-US022775.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
DR WPI; 2002-269150/31.
XX
PT Modulation of blood cell proliferation in a patient involves use of blood
PT cell regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
PS Claim 1; Page 34; 54pp; English.
XX
CC The present sequence is that of a colostrinin constituent peptide that is
CC preferred for use as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. It is classified as having
CC a beta-casein homologue precursor. Methods are claimed for: inducing a
CC cytokine in a cell by contact with an immunological regulator, where the
CC cell is present in a cell culture, a tissue, an organ or an organism, and
CC the cell is mammalian, including human; modulating an immune response in
CC a cell by contact with the immunological regulator under conditions
CC effective to induce a cytokine; modulating an immune response in a
CC patient by administering an immunological regulator under conditions
CC effective to induce a cytokine, where the immunological regulator is
CC administered topically or as part of a dietary supplement, and where the
CC immune response is specific or non specific, an interferon response or an
CC antibody response; modulating blood cell proliferation by contacting
CC blood cells with a blood cell regulator, where the blood cells are
CC present in a cell culture or an organism, are mammalian or human, and
CC where the blood cells are increased in number or differentiated; and a
CC method for modulating blood cell proliferation in a patent. A claimed
CC cytokine-inducing composition comprises a pharmaceutical carrier and an
CC active agent such as the present peptide. Cytokines induced by this
CC peptide in human leucocyte cultures include interferon-gamma, tumour
CC necrosis factor-alpha, interleukin-6 and interleukin-10. It was one of
CC the best overall inducers in almost all cytokine and blood cell
CC proliferation experiments conducted
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DQPPDVEKPDLPFQVQS 18
| | | | | | | | | | | | | | | | | |
Db 1 DQPPDVEKPDLPFQVQS 18

RESULT 7

AAE20230

ID AAE20230 standard; peptide; 18 AA.

XX

AC AAE20230;

XX

DT 18-JUN-2002 (first entry)

XX

DE Colostrinin constituent peptide #3.

XX

KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnerary.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 18

FT /note= "Optionally C-terminal amide"

XX

PN WO200213850-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022776.

XX

PR 17-AUG-2000; 2000WO-US022776.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Stanton GJ, Hughes TK, Boldogh I;

XX

DR WPI; 2002-269151/31.

XX

PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog.

XX

PS Claim 6; Page 25; 51pp; English.

XX

CC The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress level
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
CC organ, or organism; or for treating oxidative damage to the skin of a
CC patient e.g. animal or human; to modulate oxidative stress during/ after
CC a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present

CC sequence is a colostrinin constituent peptide
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPFQVQS 18
|||||
Db 1 DQPPDVEKPDLPFQVQS 18

RESULT 8

ABG67986

ID ABG67986 standard; peptide; 15 AA.

XX

AC ABG67986;

XX

DT 07-OCT-2002 (first entry)

XX

DE Human ADPI tryptic digest peptide #695.

XX

KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;

KW Alzheimer's disease-associated feature; neuroprotective;

KW Alzheimer's disease-associated protein isoform; nootropic;

KW ADPI tryptic digest peptide.

XX

OS Homo sapiens.

XX

PN WO200246767-A2.

XX

PD 13-JUN-2002.

XX

PF 29-NOV-2001; 2001WO-GB005289.

XX

PR 08-DEC-2000; 2000US-0254431P.

XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX

PI Herath HMAc, Parekh RB, Rohlf C;

XX

DR WPI; 2002-508575/54.

XX

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT comprises detecting Alzheimer disease-associated features or Alzheimer
PT disease-associated protein isoforms in brain tissue from the subject.

XX

PS Claim 7; Page 56; 427pp; English.

XX

CC The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
CC subject. The method comprises analysing a sample of brain tissue from a
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
CC disease-associated features (ADFs), whose relative abundance correlates
CC with the presence, absence, stage or severity of AD and comparing the
CC abundance of each feature with the abundance of that chosen feature in

CC brain tissue from persons free from AD. The invention also describes
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
CC brain tissue. The methods and compositions of the invention are useful
CC for the screening, diagnosis or prognosis of AD in a subject, for
CC determining the stage or severity of AD in a subject, for identifying a
CC subject at risk of developing AD, or for monitoring the effect of therapy
CC administered to a subject having AD. Antibodies capable of binding to
CC ADPIs are useful for treating or preventing AD, and for determining the
CC efficacy of a given treatment regime. An agent that modulates the
CC activity of ADPI is useful in the manufacture of a medicament for the
CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
CC human ADPI tryptic digest peptides

XX

SQ Sequence 15 AA;

Query Match 41.8%; Score 41; DB 5; Length 15;
Best Local Similarity 47.1%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 0; Indels 6; Gaps 1;

Qy 1 DQPPDVEKPDLPFQVQ 17
|||::| |:::
Db 5 DQPPDIE-----FQIR 15

RESULT 9

ADA24138

ID ADA24138 standard; peptide; 15 AA.

XX

AC ADA24138;

XX

DT 20-NOV-2003 (first entry)

XX

DE Alzheimer's disease-associated protein isoform tryptic peptide #747.

XX

KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;

KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;

KW Alzheimer's disease-associated protein isoform; ADPI.

XX

OS Homo sapiens.

XX

PN US2003064411-A1.

XX

PD 03-APR-2003.

XX

PF 10-DEC-2001; 2001US-00014340.

XX

PR 08-DEC-2000; 2000US-0254431P.

XX

PA (HERA/) HERATH H M A C.

PA (PARE/) PAREKH R B.

PA (ROHL/) ROHLFF C.

XX

PI Herath HMAc, Parekh RB, Rohlff C;

XX

DR WPI; 2003-540784/51.

XX

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,

PT involves analyzing test sample of brain tissue from subject, and
PT comparing feature in test sample with that of person(s) free from
PT Alzheimer's disease.

XX

PS Disclosure; SEQ ID NO 747; 115pp; English.

XX

CC The invention relates to a method of screening or diagnosing Alzheimer's
CC disease in a subject. The method is useful for screening, diagnosis or
CC prognosis of Alzheimer's disease in a subject for determining the stage
CC of severity of Alzheimer's disease in a subject, for identifying a
CC subject at risk of developing Alzheimer's disease, or for monitoring the
CC effect of therapy administered to a subject having Alzheimer's disease.
CC The method is also useful in treating vascular dementia, Lewy body
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potently, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.

XX

SQ Sequence 15 AA;

Query Match 41.8%; Score 41; DB 6; Length 15;
Best Local Similarity 47.1%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 0; Indels 6; Gaps 1;

Qy 1 DQPPDVEKPDLPFQVQ 17

||||:| ||::

Db 5 DQPPDIE-----FQIR 15

RESULT 10

AAR49858

ID AAR49858 standard; peptide; 16 AA.

XX

AC AAR49858;

XX

DT 25-MAR-2003 (revised)

DT 12-SEP-1994 (first entry)

XX

DE Sequence of tryptic digest peptide of bovine glial growth factor III (GGF
DE III).

XX

KW Glial growth factor; GGF III; mitogen; Schwann cell.

XX

OS Bos taurus.

XX

PN WO9404560-A1.

XX

PD 03-MAR-1994.

XX

PF 13-AUG-1993; 93WO-GB001721.

XX

PR 14-AUG-1992; 92GB-00017316.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX
 PI Goodearl ADJ, Stroobant P, Waterfield MD;
 XX
 DR WPI; 1994-083104/10.
 XX
 PT New polypeptide factor and peptide(s) from bovine pituitary - having
 PT mitogenic activity in stimulating division of Schwann cells, used for
 PT therapy, prophylaxis, diagnosis of neuro-degenerative disease, glial cell
 PT tumours, etc.
 XX
 PS Claim 32; Page 31; 44pp; English.
 XX
 CC A novel polypeptide was purified from bovine pituitaries. It has
 CC mitogenic activity stimulating the division of Schwann cells, and
 CC exhibits a mol. wt. of 43-35kD when carrying native glycosylation. It was
 CC digested with trypsin and lysylendopeptidase to obtain novel peptides
 CC AAR49858-R49866 and AAR49867-R49871 respectively. When peptides AAR49862-
 CC R49866 were sequenced to completion it was found that none of these
 CC sequences is apparently related to GGF-I or GGF-II peptide sequences. A
 CC polypeptide contg. any of the sequences in AAR49858- AAR49871 is claimed,
 CC as is DNA encoding each of the peptides. The final Lys in the sequence is
 CC bracketed. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 16 AA;

Query Match 39.8%; Score 39; DB 2; Length 16;
 Best Local Similarity 66.7%; Pred. No. 69;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VEKPDQLQPF 14
 : ||||:|
 Db 2 ISKPDLLKPF 10

RESULT 11

ABP83082

ID ABP83082 standard; peptide; 16 AA.

XX

AC ABP83082;

XX

DT 04-MAR-2003 (first entry)

XX

DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1755.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

XX

OS Homo sapiens.

XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burmer GC, Roush CL, Brown JP;
 XX
 DR WPI; 2003-046718/04.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX
 PS Claim 1; Fig 2; 523pp; English.
 XX
 CC The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 16 AA;

Query Match 39.8%; Score 39; DB 6; Length 16;
 Best Local Similarity 50.0%; Pred. No. 69;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLP 13
 :|||: | | |
 Db 5 RPPDIRKSDSSP 16

RESULT 12

AAM47777

ID AAM47777 standard; peptide; 15 AA.

XX

AC AAM47777;

XX

DT 26-FEB-2002 (first entry)

XX

DE Short chain dehydrogenase 32 peptide fragment.

XX

KW Short chain dehydrogenase 32; tumour; haemopathy; HIV infection;

KW immunological disease; inflammation; gene therapy; cytostatic;

KW haemostatic; virucide; immunomodulatory; antiinflammatory.

XX

OS Unidentified.

XX

PN CN1307114-A.

XX

PD 08-AUG-2001.

XX

PF 28-JAN-2000; 2000CN-00111584.

XX

PR 28-JAN-2000; 2000CN-00111584.

XX

PA (BODA-) BODAO GENE TECH CO LTD SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-026893/04.

XX

PT New polypeptide for treating malignant tumors and HIV infection,

PT comprises the polypeptide-short chain dehydrogenase 32 and polynucleotide

PT for coding said polypeptide.

XX

PS Example 6; Page 27 (Disclosure); 33pp; Chinese.

XX

CC The present invention relates to short chain dehydrogenase 32 (AAM47776).

CC The protein and its coding sequence are useful for treating various

CC diseases, such as malignant tumours, haemopathy, HIV infection,

CC immunological diseases and inflammations. The present sequence is an N-

CC terminal peptide fragment of the protein, which was used in an example

CC from the present invention

XX

SQ Sequence 15 AA;

Query Match 36.7%; Score 36; DB 5; Length 15;

Best Local Similarity 63.6%; Pred. No. 1.7e+02;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPDVEKPDLP 13

||||| | |

Db 5 PPDVEGDDCLP 15

RESULT 13

ABG67771

ID ABG67771 standard; peptide; 12 AA.

XX

AC ABG67771;

XX

DT 07-OCT-2002 (first entry)

XX

DE Human ADPI tryptic digest peptide #480.

XX

KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;

KW Alzheimer's disease-associated feature; neuroprotective;

KW Alzheimer's disease-associated protein isoform; nootropic;

KW ADPI tryptic digest peptide.

XX

OS Homo sapiens.

XX

PN WO200246767-A2.

XX

PD 13-JUN-2002.

XX

PF 29-NOV-2001; 2001WO-GB005289.

XX

PR 08-DEC-2000; 2000US-0254431P.

XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX

PI Herath HMAc, Parekh RB, Rohlf C;

XX

DR WPI; 2002-508575/54.

XX

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT comprises detecting Alzheimer disease-associated features or Alzheimer
PT disease-associated protein isoforms in brain tissue from the subject.

XX

PS Claim 7; Page 55; 427pp; English.

XX

CC The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
CC subject. The method comprises analysing a sample of brain tissue from a
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
CC disease-associated features (ADFs), whose relative abundance correlates
CC with the presence, absence, stage or severity of AD and comparing the
CC abundance of each feature with the abundance of that chosen feature in
CC brain tissue from persons free from AD. The invention also describes
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
CC brain tissue. The methods and compositions of the invention are useful
CC for the screening, diagnosis or prognosis of AD in a subject, for
CC determining the stage or severity of AD in a subject, for identifying a
CC subject at risk of developing AD, or for monitoring the effect of therapy
CC administered to a subject having AD. Antibodies capable of binding to
CC ADPIs are useful for treating or preventing AD, and for determining the
CC efficacy of a given treatment regime. An agent that modulates the
CC activity of ADPI is useful in the manufacture of a medicament for the
CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
CC human ADPI tryptic digest peptides

XX

SQ Sequence 12 AA;

Query Match 35.7%; Score 35; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLO 12
|| | |||:
Db 3 PPSAEYPDLR 12

RESULT 14

ADA23910

ID ADA23910 standard; peptide; 12 AA.

XX

AC ADA23910;

XX

DT 20-NOV-2003 (first entry)

XX

DE Alzheimer's disease-associated protein isoform tryptic peptide #519.

XX

KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;

KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;

KW Alzheimer's disease-associated protein isoform; ADPI.

XX

OS Homo sapiens.

XX

PN US2003064411-A1.

XX

PD 03-APR-2003.

XX

PF 10-DEC-2001; 2001US-00014340.

XX

PR 08-DEC-2000; 2000US-0254431P.

XX

PA (HERA/) HERATH H M A C.

PA (PARE/) PAREKH R B.

PA (ROHL/) ROHLFF C.

XX

PI Herath HMAc, Parekh RB, Rohlff C;

XX

DR WPI; 2003-540784/51.

XX

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,

PT involves analyzing test sample of brain tissue from subject, and

PT comparing feature in test sample with that of person(s) free from

PT Alzheimer's disease.

XX

PS Disclosure; SEQ ID NO 519; 115pp; English.

XX

CC The invention relates to a method of screening or diagnosing Alzheimer's

CC disease in a subject. The method is useful for screening, diagnosis or

CC prognosis of Alzheimer's disease in a subject for determining the stage

CC of severity of Alzheimer's disease in a subject, for identifying a

CC subject at risk of developing Alzheimer's disease, or for monitoring the

CC effect of therapy administered to a subject having Alzheimer's disease.

CC The method is also useful in treating vascular dementia, Lewy body

CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or

CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potently, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.

XX

SQ Sequence 12 AA;

Query Match 35.7%; Score 35; DB 6; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLQ 12
|| | |||:
Db 3 PPSAEYPDLR 12

RESULT 15

AAB26624

ID AAB26624 standard; peptide; 13 AA.

XX

AC AAB26624;

XX

DT 22-JAN-2001 (first entry)

XX

DE Partial sequence #24 of Breast Cancer-Associated Protein Isoform.

XX

KW BPI; breast cancer-associated protein isoform; gene therapy;
KW breast cancer.

XX

OS Homo sapiens.

XX

PN WO200055628-A1.

XX

PD 21-SEP-2000.

XX

PF 13-MAR-2000; 2000WO-GB000908.

XX

PR 12-MAR-1999; 99GB-00005817.

XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX

PI Amess B, Townsend RR, Parekh RB, Waterfield MD, O'hare MJ;

XX

DR WPI; 2000-602142/57.

XX

PT Screening, diagnosis of breast cancer and monitoring the effectiveness of
PT breast cancer therapy, involves detecting breast cancer-associated
PT features and breast cancer-associated protein isoforms.

XX

PS Disclosure; Page 14; 86pp; English.

XX

CC The present invention relates to the screening, diagnosis and prognosis
CC of breast cancer, for monitoring the effectiveness of breast cancer
CC treatment in a human, comprising identifying the presence or absence of
CC breast cancer-associated features (BF) or breast cancer-associated

CC protein isoforms (BPIs). Antibodies derived from BF and BPIs may be
CC useful for the treatment and screening of breast cancer, in particular.
CC metastatic breast cancer. The present sequence is the partial sequence of
CC a BPI
XX
SQ Sequence 13 AA;

Query Match 35.7%; Score 35; DB 3; Length 13;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKPD LQ 12
|| | |||:
Db 4 PPSAEY PDLR 13

RESULT 16

ABB97740

ID ABB97740 standard; peptide; 13 AA.

XX

AC ABB97740;

XX

DT 11-JUL-2002 (first entry)

XX

DE Human procathepsin W epitope peptide #120.

XX

KW Human; procathepsin W; cathepsin W; monoclonal antibody; epitope.

XX

OS Homo sapiens.

XX

PN WO200226831-A1.

XX

PD 04-APR-2002.

XX

PF 09-JUL-2001; 2001WO-EP007877.

XX

PR 29-SEP-2000; 2000DE-01048727.

XX

PA (LABS-) LABSOFT DIAGNOSTICS AG.

XX

PI Weber E;

XX

DR WPI; 2002-330095/36.

XX

PT New hybridoma cell lines that produces antibodies specific for human

PT cathepsin W, useful e.g. for diagnosis, therapy and drug targeting.

XX

PS Disclosure; Fig 1; 23pp; German.

XX

CC The present invention relates to hybridoma cell lines that produce
CC monoclonal antibodies directed against a defined epitope of human
CC (pro)cathepsin W, which are produced by fusing myeloma cells with spleen
CC cells from an animal that has been immunised with recombinant
CC procathepsin W. The antibodies produced are useful for analysis,
CC diagnosis (detection of human (pro)cathepsin W), purification of
CC (pro)cathepsin W (also for clarifying processing of the precursor and
CC functional significance of the mature protein), for drug targeting and

CC for therapeutic use. The present sequence is an epitope of human
CC procathepsin W
XX
SQ Sequence 13 AA;

Query Match 34.7%; Score 34; DB 5; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13
|:|:|:|
Db 3 VQKPDMPK 10

RESULT 17

ABB97739

ID ABB97739 standard; peptide; 13 AA.

XX

AC ABB97739;

XX

DT 11-JUL-2002 (first entry)

XX

DE Human procathepsin W epitope peptide #119.

XX

KW Human; procathepsin W; cathepsin W; monoclonal antibody; epitope.

XX

OS Homo sapiens.

XX

PN WO200226831-A1.

XX

PD 04-APR-2002.

XX

PF 09-JUL-2001; 2001WO-EP007877.

XX

PR 29-SEP-2000; 2000DE-01048727.

XX

PA (LABS-) LABSOFT DIAGNOSTICS AG.

XX

PI Weber E;

XX

DR WPI; 2002-330095/36.

XX

PT New hybridoma cell lines that produces antibodies specific for human

PT cathepsin W, useful e.g. for diagnosis, therapy and drug targeting.

XX

PS Disclosure; Fig 1; 23pp; German.

XX

CC The present invention relates to hybridoma cell lines that produce
CC monoclonal antibodies directed against a defined epitope of human
CC (pro)cathepsin W, which are produced by fusing myeloma cells with spleen
CC cells from an animal that has been immunised with recombinant
CC procathepsin W. The antibodies produced are useful for analysis,
CC diagnosis (detection of human (pro)cathepsin W), purification of
CC (pro)cathepsin W (also for clarifying processing of the precursor and
CC functional significance of the mature protein), for drug targeting and
CC for therapeutic use. The present sequence is an epitope of human
CC procathepsin W

XX
SQ Sequence 13 AA;

Query Match 34.7%; Score 34; DB 5; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKPDLP 13
|:|:|:|
Db 6 VQKPDMP 13

RESULT 18
AAB21134

ID AAB21134 standard; peptide; 15 AA.

XX

AC AAB21134;

XX

DT 19-JAN-2001 (first entry)

XX

DE Src homology 3 domain binding peptide #11.

XX

KW Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.

XX

OS Synthetic.

XX

PN WO200047607-A1.

XX

PD 17-AUG-2000.

XX

PF 12-FEB-2000; 2000WO-KR000107.

XX

PR 12-FEB-1999; 99AU-00008643.

PR 02-JUN-1999; 99KR-00020282.

XX

PA (YOON/) YOON J H.

PA (HANY/) HAN Y T.

XX

PI Yoon JH, Han YT, Lee KY;

XX

DR WPI; 2000-533010/48.

XX

PT Synthetic peptides useful for treating cancers and immunosuppressive
PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3
PT motifs of Src family kinase proteins.

XX

PS Claim 3; Page 35; 40pp; English.

XX

CC The present sequence is a synthetic peptide which has a high affinity for
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC involved in signal transduction pathways, and this peptide can be used to
CC inhibit these, by disrupting protein-protein interactions, in the
CC treatment of cancer, particularly hepatocellular carcinoma, cervical
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-
CC associated diseases

XX

SQ Sequence 15 AA;

Query Match 33.7%; Score 33; DB 3; Length 15;
Best Local Similarity 41.7%; Pred. No. 4.7e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDQL 12
::|| | || :
Db 2 ERPPPVPNPDIY 13

RESULT 19

AAY41624

ID AAY41624 standard; peptide; 18 AA.

XX

AC AAY41624;

XX

DT 02-DEC-1999 (first entry)

XX

DE Mammalian ion channel proline rich motif containing peptide #18.

XX

KW SH3 domain; binding motif; potassium channel; protein tyrosine kinase;
KW proline rich.

XX

OS Rattus sp.

XX

PN US5955259-A.

XX

PD 21-SEP-1999.

XX

PF 19-DEC-1996; 96US-00769745.

XX

PR 19-DEC-1996; 96US-00769745.

XX

PA (UYBR-) UNIV BRANDEIS.

XX

PI Holmes TC, Levitan IB;

XX

DR WPI; 1999-560490/47.

XX

PT Identification of compounds that modulate potassium ion channel binding
PT with protein tyrosine kinase SH3 domains.

XX

PS Disclosure; Col 8; 18pp; English.

XX

CC A method has been developed for determining if a compound modulates the
CC binding of a potassium ion channel to the SH3 domain of a protein
CC tyrosine kinase by contacting the channel with a polypeptide comprising
CC the SH3 domain and the compound to be assessed and measuring channel-SH3
CC binding. The method is useful for assessing the ability of a compound to
CC modulate the formation of channel-SH3 domain complexes to improve the
CC understanding of mechanisms of potassium channel blockage and assess the
CC ability of potential therapeutics to inhibit blockage. AAY41607 to
CC AAY41644 represent mammalian ion channel peptides with proline-rich
CC motifs

XX

SQ Sequence 18 AA;

Query Match 33.7%; Score 33; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDILQP 13
|||: |||
Db 6 QPPESSPPPLLP 17

RESULT 20

AAE34138

ID AAE34138 standard; peptide; 18 AA.

XX

AC AAE34138;

XX

DT 02-MAY-2003 (first entry)

XX

DE T-cell stimulatory gluten peptide #17.

XX

KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;

KW food-related immune enteropathy; tropical sprue; gluten sensitivity;

KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.

XX

OS Unidentified.

XX

PN WO200283722-A2.

XX

PD 24-OCT-2002.

XX

PF 11-APR-2002; 2002WO-NL000235.

XX

PR 12-APR-2001; 2001EP-00201377.

PR 16-NOV-2001; 2001EP-00204383.

XX

PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

XX

PI Drijfhout JW, Koning F, Mcadam SN, Sollid LM;

XX

DR WPI; 2003-093000/08.

XX

PT Novel isolated or recombinant human leukocyte antigen-DQ restricted T-

PT cell receptor for treating food-related immune enteropathy such as celiac

PT sprue, tropical sprue, giardiasis and food allergies of childhood.

XX

PS Disclosure; Fig 2; 64pp; English.

XX

CC The present invention relates to novel isolated or recombinant human

CC leukocyte antigen (HLA)-DQ restricted T-cell receptor or its functional

CC equivalent and/or fragment, capable of recognising a prolamine-derived

CC peptide. The invention relates to recombinant or synthetic prolamine

CC derived peptides involved in food-related immune enteropathy. The

CC pharmaceutical composition is useful to treat food-related immune

CC enteropathies such as celiac sprue, tropical sprue, giardiasis or food

CC allergies of childhood. It is useful to induce tolerance, treat gluten-

CC sensitivity and to eliminate gluten-sensitive T-cells. Sequences of the

CC invention are useful to decrease the amount of toxic prolamine-derived

CC peptides in food or food components and to select and/or breed a cereal.
CC The cereal is useful for inclusion in a diet for a gluten sensitive
CC individual. Blocking substances are useful to decrease the binding of HLA
CC -DQ restricted T-cell receptor to a prolamine-derived peptide involved in
CC food-related immune enteropathy for depletion of T-cells bearing the HLA-
CC DQ restricted T-cell receptor. The present sequence is T-cell stimulatory
CC gluten peptide. This sequence is used in the invention

XX

SQ Sequence 18 AA;

Query Match 33.7%; Score 33; DB 6; Length 18;
Best Local Similarity 46.7%; Pred. No. 5.6e+02;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPQPFQVQ 17
|| | ||| |
Db 2 PPQQPYPPQPPFPSQ 16

RESULT 21

AAE34142

ID AAE34142 standard; peptide; 18 AA.

XX

AC AAE34142;

XX

DT 02-MAY-2003 (first entry)

XX

DE T-cell stimulatory gluten peptide #21.

XX

KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;

KW food-related immune enteropathy; tropical sprue; gluten sensitivity;

KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.

XX

OS Unidentified.

XX

PN WO200283722-A2.

XX

PD 24-OCT-2002.

XX

PF 11-APR-2002; 2002WO-NL000235.

XX

PR 12-APR-2001; 2001EP-00201377.

PR 16-NOV-2001; 2001EP-00204383.

XX

PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

XX

PI Drijfhout JW, Koning F, Mcadam SN, Sollid LM;

XX

DR WPI; 2003-093000/08.

XX

PT Novel isolated or recombinant human leukocyte antigen-DQ restricted T-

PT cell receptor for treating food-related immune enteropathy such as celiac

PT sprue, tropical sprue, giardiasis and food allergies of childhood.

XX

PS Disclosure; Fig 2; 64pp; English.

XX

CC The present invention relates to novel isolated or recombinant human

CC leukocyte antigen (HLA)-DQ restricted T-cell receptor or its functional
 CC equivalent and/or fragment, capable of recognising a prolamine-derived
 CC peptide. The invention relates to recombinant or synthetic prolamine
 CC derived peptides involved in food-related immune enteropathy. The
 CC pharmaceutical composition is useful to treat food-related immune
 CC enteropathies such as celiac sprue, tropical sprue, giardiasis or food
 CC allergies of childhood. It is useful to induce tolerance, treat gluten-
 CC sensitivity and to eliminate gluten-sensitive T-cells. Sequences of the
 CC invention are useful to decrease the amount of toxic prolamine-derived
 CC peptides in food or food components and to select and/or breed a cereal.
 CC The cereal is useful for inclusion in a diet for a gluten sensitive
 CC individual. Blocking substances are useful to decrease the binding of HLA
 CC -DQ restricted T-cell receptor to a prolamine-derived peptide involved in
 CC food-related immune enteropathy for depletion of T-cells bearing the HLA-
 CC DQ restricted T-cell receptor. The present sequence is T-cell stimulatory
 CC gluten peptide. This sequence is used in the invention
 XX
 SQ Sequence 18 AA;

Query Match 33.7%; Score 33; DB 6; Length 18;
 Best Local Similarity 46.7%; Pred. No. 5.6e+02;
 Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPFQVQ 17
 || | || |
 Db 2 PPQQPYPPQPPFPSQ 16

RESULT 22

AAE34133

ID AAE34133 standard; peptide; 18 AA.

XX

AC AAE34133;

XX

DT 02-MAY-2003 (first entry)

XX

DE T-cell stimulatory gluten peptide #12.

XX

KW Human leukocyte antigen; HLA; T-cell receptor; giardiasis; celiac sprue;

KW food-related immune enteropathy; tropical sprue; gluten sensitivity;

KW food allergy; protozoacide; antiinflammatory; immunosuppressive; gluten.

XX

OS Unidentified.

XX

PN WO200283722-A2.

XX

PD 24-OCT-2002.

XX

PF 11-APR-2002; 2002WO-NL000235.

XX

PR 12-APR-2001; 2001EP-00201377.

PR 16-NOV-2001; 2001EP-00204383.

XX

PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

XX

PI Drijfhout JW, Koning F, Mcadam SN, Sollid LM;

XX

DR WPI; 2003-093000/08.

XX

PT Novel isolated or recombinant human leukocyte antigen-DQ restricted T-cell receptor for treating food-related immune enteropathy such as celiac sprue, tropical sprue, giardiasis and food allergies of childhood.

XX

PS Disclosure; Fig 2; 64pp; English.

XX

CC The present invention relates to novel isolated or recombinant human leukocyte antigen (HLA)-DQ restricted T-cell receptor or its functional equivalent and/or fragment, capable of recognising a prolamine-derived peptide. The invention relates to recombinant or synthetic prolamine derived peptides involved in food-related immune enteropathy. The pharmaceutical composition is useful to treat food-related immune enteropathies such as celiac sprue, tropical sprue, giardiasis or food allergies of childhood. It is useful to induce tolerance, treat gluten-sensitivity and to eliminate gluten-sensitive T-cells. Sequences of the invention are useful to decrease the amount of toxic prolamine-derived peptides in food or food components and to select and/or breed a cereal. The cereal is useful for inclusion in a diet for a gluten sensitive individual. Blocking substances are useful to decrease the binding of HLA-DQ restricted T-cell receptor to a prolamine-derived peptide involved in food-related immune enteropathy for depletion of T-cells bearing the HLA-DQ restricted T-cell receptor. The present sequence is T-cell stimulatory gluten peptide. This sequence is used in the invention

XX

SQ Sequence 18 AA;

Query Match 33.7%; Score 33; DB 6; Length 18;
Best Local Similarity 46.7%; Pred. No. 5.6e+02;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPFQVQ 17
|| | ||| |
Db 2 PPQQPYPPQPPFQS 16

RESULT 23

AAB21124

ID AAB21124 standard; peptide; 11 AA.

XX

AC AAB21124;

XX

DT 19-JAN-2001 (first entry)

XX

DE Src homology 3 domain binding peptide #1.

XX

KW Src homology domain 3; SH3; protein-protein interaction; cancer;
KW signal transduction inhibition; immune suppression-associated disease.

XX

OS Synthetic.

XX

PN WO200047607-A1.

XX

PD 17-AUG-2000.

XX

PF 12-FEB-2000; 2000WO-KR000107.

XX
 PR 12-FEB-1999; 99AU-00008643.
 PR 02-JUN-1999; 99KR-00020282.
 XX
 PA (YOON/) YOON J H.
 PA (HANY/) HAN Y T.
 XX
 PI Yoon JH, Han YT, Lee KY;
 XX
 DR WPI; 2000-533010/48.
 XX
 PT Synthetic peptides useful for treating cancers and immunosuppressive
 PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3
 PT motifs of Src family kinase proteins.
 XX
 PS Claim 3; Page 32; 40pp; English.
 XX
 CC The present sequence is a synthetic peptide which has a high affinity for
 CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
 CC involved in signal transduction pathways, and this peptide can be used to
 CC inhibit these, by disrupting protein-protein interactions, in the
 CC treatment of cancer, particularly hepatocellular carcinoma, cervical
 CC cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-
 CC associated diseases
 XX
 SQ Sequence 11 AA;

Query Match 32.7%; Score 32; DB 3; Length 11;
 Best Local Similarity 50.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPD 10
 :||| | ||
 Db 2 ERPPVPNPDP 11

RESULT 24
 AAB21133
 ID AAB21133 standard; peptide; 11 AA.
 XX
 AC AAB21133;
 XX
 DT 19-JAN-2001 (first entry)
 XX
 DE Src homology 3 domain binding peptide #10.
 XX
 KW Src homology domain 3; SH3; protein-protein interaction; cancer;
 KW signal transduction inhibition; immune suppression-associated disease.
 XX
 OS Synthetic.
 XX
 PN WO200047607-A1.
 XX
 PD 17-AUG-2000.
 XX
 PF 12-FEB-2000; 2000WO-KR000107.
 XX

PR 12-FEB-1999; 99AU-00008643.
PR 02-JUN-1999; 99KR-00020282.

XX

PA (YOON/) YOON J H.

PA (HANY/) HAN Y T.

XX

PI Yoon JH, Han YT, Lee KY;

XX

DR WPI; 2000-533010/48.

XX

PT Synthetic peptides useful for treating cancers and immunosuppressive
PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3
PT motifs of Src family kinase proteins.

XX

PS Claim 3; Page 35; 40pp; English.

XX

CC The present sequence is a synthetic peptide which has a high affinity for
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are
CC involved in signal transduction pathways, and this peptide can be used to
CC inhibit these, by disrupting protein-protein interactions, in the
CC treatment of cancer, particularly hepatocellular carcinoma, cervical
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-
CC associated diseases

XX

SQ Sequence 11 AA;

Query Match 32.7%; Score 32; DB 3; Length 11;

Best Local Similarity 50.0%; Pred. No. 4.7e+02;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPD 10

::||| | ||

Db 2 ERPPFVNPND 11

RESULT 25

AAU01841

ID AAU01841 standard; peptide; 17 AA.

XX

AC AAU01841;

XX

DT 07-SEP-2001 (first entry)

XX

DE Wheat peptide antagonist for A-gliadin 57-73 QE65 #3.

XX

KW Wheat; A-gliadin; 57-75 QE65; coeliac disease; gluten intolerance;

KW T-cell binding; antagonist; transglutaminase; transgenic plant.

XX

OS Triticum aestivum.

XX

PN WO200125793-A2.

XX

PD 12-APR-2001.

XX

PF 02-OCT-2000; 2000WO-GB003760.

XX

PR 01-OCT-1999; 99GB-00023306.

XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Anderson RP, Hill AVS, Jewell DP;
XX
DR WPI; 2001-300179/31.
XX
PT Diagnosing coeliac disease or susceptibility to the disease in an
PT individual, by detecting in vitro or in vivo T cells which bind
PT immunodominant T cell epitope obtained from naturally occurring homolog
PT of gliadin.
XX
PS Example 11; Page 58; 107pp; English.
XX
CC The sequence represents a gliadin peptide corresponding to A-gliadin 57-
CC 73 which is naturally polymorphic in that region and is antagonistic to A
CC -gliadin 57-73 QE65 interferon gamma ELISpot (not defined) response. The
CC peptides of the invention are used to test mammalian (preferably human)
CC susceptibility to coeliac disease (gluten intolerance). The peptides are
CC contacted with a blood sample and T cell recognition measured, a positive
CC T-cell recognition indicating a susceptibility to coeliac disease. The
CC peptides are useful for inducing tolerance in an individual and
CC antagonists to the peptides are useful for treating or preventing coeliac
CC disease in an individual and for producing an antibody specific to them
CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15
CC amino acids in length) whose wild-type sequence can be modified by
CC transglutaminase to a sequence that comprises the epitope, but which has
CC been modified in such a way that it does not contain sequence which can
CC be modified by transglutaminase to a sequence that comprise the epitope
CC is useful for decreasing the ability of gliadin protein to cause Coeliac
CC disease. Nucleic acids encoding proteins antagonistic to the T-cell
CC binding of the epitopes are useful for obtaining a transgenic plant cell
CC or seed and for the production of a protein. The resultant crop plant is
CC useful for obtaining a product of a wheat plant, especially grain, which
CC is optionally processed into flour or another grain product. Food
CC comprising the antagonistic protein is useful instead of a wild-type
CC gliadin
XX
SQ Sequence 17 AA;

Query Match 32.7%; Score 32; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPDVEKPDLP 13
||:: | ||
Db 7 PPELPYPQTQP 17

RESULT 26
AAU01840
ID AAU01840 standard; peptide; 17 AA.
XX
AC AAU01840;
XX
DT 07-SEP-2001 (first entry)
XX

DE Wheat peptide antagonist for A-gliadin 57-73 QE65 #2.
 XX
 KW Wheat; A-gliadin; 57-75 QE65; coeliac disease; gluten intolerance;
 KW T-cell binding; antagonist; transglutaminase; transgenic plant.
 XX
 OS Triticum aestivum.
 XX
 PN WO200125793-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 02-OCT-2000; 2000WO-GB003760.
 XX
 PR 01-OCT-1999; 99GB-00023306.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 XX
 PI Anderson RP, Hill AVS, Jewell DP;
 XX
 DR WPI; 2001-300179/31.
 XX
 PT Diagnosing coeliac disease or susceptibility to the disease in an
 PT individual, by detecting in vitro or in vivo T cells which bind
 PT immunodominant T cell epitope obtained from naturally occurring homolog
 PT of gliadin.
 XX
 PS Example 11; Page 58; 107pp; English.
 XX
 CC The sequence represents a gliadin peptide corresponding to A-gliadin 57-
 CC 73 which is naturally polymorphic in that region and is antagonistic to A
 CC -gliadin 57-73 QE65 interferon gamma ELISpot (not defined) response. The
 CC peptides of the invention are used to test mammalian (preferably human)
 CC susceptibility to coeliac disease (gluten intolerance). The peptides are
 CC contacted with a blood sample and T cell recognition measured, a positive
 CC T-cell recognition indicating a susceptibility to coeliac disease. The
 CC peptides are useful for inducing tolerance in an individual and
 CC antagonists to the peptides are useful for treating or preventing coeliac
 CC disease in an individual and for producing an antibody specific to them
 CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15
 CC amino acids in length) whose wild-type sequence can be modified by
 CC transglutaminase to a sequence that comprises the epitope, but which has
 CC been modified in such a way that it does not contain sequence which can
 CC be modified by transglutaminase to a sequence that comprise the epitope
 CC is useful for decreasing the ability of gliadin protein to cause Coeliac
 CC disease. Nucleic acids encoding proteins antagonistic to the T-cell
 CC binding of the epitopes are useful for obtaining a transgenic plant cell
 CC or seed and for the production of a protein. The resultant crop plant is
 CC useful for obtaining a product of a wheat plant, especially grain, which
 CC is optionally processed into flour or another grain product. Food
 CC comprising the antagonistic protein is useful instead of a wild-type
 CC gliadin
 XX
 SQ Sequence 17 AA;

Query Match 32.7%; Score 32; DB 4; Length 17;
 Best Local Similarity 45.5%; Pred. No. 7.4e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLP 13
||:: | ||
Db 7 PPELPYPQTQP 17

RESULT 27

AAW38909

ID AAW38909 standard; peptide; 18 AA.

XX

AC AAW38909;

XX

DT 27-MAR-1998 (first entry)

XX

DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.

XX

KW Cortactin; SH3 domain; binding peptide; Src homology region 3;

KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;

KW PLCgamma; p53bp2; Crk; Yes; Grb2.

XX

OS Synthetic.

XX

PN WO9730074-A1.

XX

PD 21-AUG-1997.

XX

PF 14-FEB-1997; 97WO-US002298.

XX

PR 16-FEB-1996; 96US-00602999.

XX

PA (CYTO-) CYTOGEN CORP.

PA (UYNC-) UNIV NORTH CAROLINA.

XX

PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;

PI Rider JE;

XX

DR WPI; 1997-424972/39.

XX

PT Src homology region 3 binding peptide - used to activate Src tyrosine
PT kinase(s) and to stimulate immune response by increasing production of
PT certain lymphokine(s), e.g. interleukin-1.

XX

PS Claim 22; Page 90; 13lpp; English.

XX

CC The present sequence represents a peptide which resembles a Src homology
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain
CC of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which
CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain
CC of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
CC bind the amino-terminal SH3 domain of Grb2. The purified binding peptides
CC can be used in the method to identify inhibitors of their binding to
CC their respective SH3 domains, which could be used to modulate the
CC pharmacological activity of proteins or polypeptide containing the SH3
CC domain. The peptides can also be used to activate Src or Src-related

CC protein tyrosine kinases, to stimulate the immune response by increasing
CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha
CC and interleukin-1, or to deliver a conjugated molecule to certain
CC cellular compartments containing Src or Src related proteins

XX

SQ Sequence 18 AA;

Query Match 32.7%; Score 32; DB 2; Length 18;
Best Local Similarity 43.8%; Pred. No. 7.8e+02;
Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLPFQVQ 17
||| | || |
Db 3 QPPYFPPPPYQPIYPQ 18

RESULT 28

AAG97089

ID AAG97089 standard; peptide; 10 AA.

XX

AC AAG97089;

XX

DT 18-SEP-2001 (first entry)

XX

DE Human complementary peptide, SEQ ID NO: 3283.

XX

KW Human; complementary peptide; ligand; drug discovery; drug design.

XX

OS Homo sapiens.

XX

PN WO200142277-A2.

XX

PD 14-JUN-2001.

XX

PF 13-DEC-2000; 2000WO-GB004776.

XX

PR 13-DEC-1999; 99GB-00029464.

XX

PA (PROT-) PROTEOM LTD.

XX

PI Roberts GW, Heal JR;

XX

DR WPI; 2001-408419/43.

XX

PT A set of peptide ligands consisting of specific complementary peptides to
PT proteins encoded by genes of the human genome, useful in an assay for
PT screening and identifying of one or more novel peptides which are drug
PT candidates or pro-drugs.

XX

PS Example 4; Page 515; 646pp; English.

XX

CC The invention relates to a set of complementary peptide ligands generated
CC from the human genome. The complementary peptides interact with their
CC relevant target proteins encoded in the human genome. They can be used as
CC reagents in drug discovery and as lead ligands to facilitate drug design
CC and development. The present sequence is a complementary peptide provided
CC in the specification

XX
SQ Sequence 10 AA;

Query Match 31.6%; Score 31; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPDVEKP 9
|||:|
Db 3 PPTVQKP 9

RESULT 29

AAW17451

ID AAW17451 standard; peptide; 11 AA.

XX

AC AAW17451;

XX

DT 17-JUN-1997 (first entry)

XX

DE Consensus antibacterial peptide from Podisus maculiventris.

XX

KW Podisus maculiventris; proline-rich; pathogenic; bacteria; bug;

KW Gram negative; plant treatment.

XX

OS Podisus maculiventris.

XX

FH Key Location/Qualifiers

FT Misc-difference 11

FT /note= "X= a peptide residue comprising at least one
FT tripeptide Pro-Arg-Pro motif"

XX

PN FR2732345-A1.

XX

PD 04-OCT-1996.

XX

PF 03-APR-1995; 95FR-00004130.

XX

PR 03-APR-1995; 95FR-00004130.

XX

PA (RHON) RHONE POULENC AGROCHIMIE.

XX

PI Bulet P, Hoffman J, Hetru C, Tchernych S;

XX

DR WPI; 1996-457711/46.

XX

PT Proline-rich antibacterial peptide(s) from Podisus maculiventris - esp.

PT useful to protect plants against pathogenic bacteria, also for

PT antibacterial therapy of animals.

XX

PS Claim 1; Page 14; 16pp; English.

XX

CC AAW17451 is a generic sequence of an antibacterial peptide from the bug

CC Podisus maculoventris. The proline-rich peptide has antibacterial

CC activity against gram negative bacteria. It is useful for protecting

CC plants against pathogenic bacteria, but could also be used for

CC antibacterial therapy of animals, including humans. For specific examples

CC see AAW09375-W09378

XX

SQ Sequence 11 AA;

Query Match 31.6%; Score 31; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 6.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VEKPDLP 13

|:|:|:|

Db 1 VDKPDYRP 8

RESULT 30

ABP61522

ID ABP61522 standard; peptide; 11 AA.

XX

AC ABP61522;

XX

DT 02-OCT-2002 (first entry)

XX

DE Human KRPI tryptic digest peptide #34.

XX

KW Human; tryptic digest peptide; KRPI; kidney response; KR;

KW nephrotropic kidney response-associated protein isoform; gene therapy;

KW antisense therapy; kidney function; tubular nephritis; renal failure;

KW nephron cell metabolic pathway modulation; glomerular necrosis;

KW papillary necrosis.

XX

OS Homo sapiens.

XX

PN WO200254081-A2.

XX

PD 11-JUL-2002.

XX

PF 24-DEC-2001; 2001WO-GB005777.

XX

PR 29-DEC-2000; 2000US-0260392P.

XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX

PI Holt GD, Kelly MD, Kennedy SJ, Moyses C;

XX

DR WPI; 2002-583637/62.

XX

PT Screening, diagnosis or prognosis of kidney response in subject, by

PT detecting kidney response-associated features or kidney response-

PT associated protein isoforms in body fluid or tissue from subject.

XX

PS Disclosure; Page 39; 168pp; English.

XX

CC The invention relates to a novel method for the screening, diagnosis or

CC prognosis of kidney response (KR). The method of the invention has

CC nephrotropic activity, and may have a use in gene therapy or antisense

CC therapy. The method is useful for the screening, diagnosis or prognosis

CC of KR in a subject, for determining the stage or severity of KR in a

CC subject, for identifying a subject at risk of developing KR, or for

CC monitoring the effect of therapy administered to a subject with KR. An
CC alternative method of the invention is useful for screening agents that
CC interact with one or more of the kidney response-associated protein
CC isoforms (KRPIs). The kidney response includes alterations in kidney
CC function, any phase of nephron cell metabolic pathway modulation,
CC glomerular/proximal tubular nephritis, glomerular/papillary necrosis,
CC acute and chronic renal failure, and end stage renal disease. The
CC sequences shown in ABP61514-ABP61787 represent tryptic digest peptides of
CC the KRPIs of the invention

XX

SQ Sequence 11 AA;

Query Match 31.6%; Score 31; DB 5; Length 11;
Best Local Similarity 55.6%; Pred. No. 6.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 EKPDLQPFQ 15
: |:| |||
Db 2 DNPNLPPFQ 10

RESULT 31

AAW45819

ID AAW45819 standard; peptide; 15 AA.

XX

AC AAW45819;

XX

DT 25-JUN-1998 (first entry)

XX

DE Peptide recognised by anti HSV-2 glycoprotein G (gG) antibody E5.

XX

KW Glycoprotein G; herpes simplex virus type 2; HSV-2 gG; anti-gG2;

KW HSV-2 infection; vaccine; diagnosis.

XX

OS Synthetic.

XX

PN WO9803544-A1.

XX

PD 29-JAN-1998.

XX

PF 24-JUL-1997; 97WO-GB002003.

XX

PR 24-JUL-1996; 96GB-00015533.

XX

PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX

PI Grabowska AM, Irving WL, Laing P;

XX

DR WPI; 1998-120696/11.

XX

PT Polypeptide antigen of Herpes simplex virus 2 glycoprotein G - used to
PT create antibodies for treating HSV-2 infection.

XX

PS Disclosure; Page 36; 63pp; English.

XX

CC This sequence is shown in the specification. The invention relates to a
CC novel polypeptide which comprises 3-20 amino acids, or a peptidomimetic

CC analogue of it where the analogue is at least partly non-peptide in
 CC nature and the analogue has a length equivalent to that determined by 3-
 CC 20 amino acid residues, which is a sequence not naturally occurring in
 CC the native sequence of the Herpes simplex virus glycoprotein G (HSV-2 gG
 CC protein), and has one of the following sequences: (X)n- alpha - beta -
 CC gamma -(Y)m (I); or (X)n- delta - epsilon - theta -(Y)m (II); n = 0 or an
 CC integer; m = 0 or an integer; n+m at most 17; alpha is E or may be
 CC substituted in order of preference by D greater than T greater than S
 CC greater than Q greater than N; beta is H; gamma is R or may be
 CC substituted in order of preference by R greater than A or L greater than
 CC T or P; epsilon is P; theta is L or may be substituted in order of
 CC preference by B or Y; and X or Y are positively charged, negatively
 CC charged or neutral amino acids or peptidomimetics thereof. The
 CC polypeptide can be used in vaccine compositions, which can be used to
 CC prevent HSV-2 infection. It can also be used to test for the presence of
 CC type-specific HSV-2 gG2 antibodies in a fluid. This test can be used to
 CC diagnose HSV-2 infection
 XX
 SQ Sequence 15 AA;

Query Match 31.6%; Score 31; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 9e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPD 10
 | || : ||
 Db 5 DPPPPLHAPD 14

RESULT 32
 AAW45614

ID AAW45614 standard; peptide; 15 AA.

XX

AC AAW45614;

XX

DT 24-JUN-1998 (first entry)

XX

DE Peptide recognised by anti HSV-2 glycoprotein G (gG) antibody E5.

XX

KW Antigenic peptide; herpes simplex virus type 2; HSV-2; glycoprotein-G;
 KW gG; vaccine; HSV-2 infection; diagnose.

XX

OS Synthetic.

XX

PN WO9803543-A1.

XX

PD 29-JAN-1998.

XX

PF 24-JUL-1997; 97WO-GB001990.

XX

PR 24-JUL-1996; 96GB-00015533.

XX

PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX

PI Grabowska AM, Irving WL, Laing P;

XX

DR WPI; 1998-120695/11.

XX
PT Polypeptide antigen of Herpes simplex virus 2 glycoprotein G - used to
PT create antibodies for treating HSV-2 infection.
XX
PS Disclosure; Page 32; 6lpp; English.
XX
CC Peptides AAW45608-15 represent antigenic peptides that are recognised by
CC antibodies against the herpes simplex virus type 2 (HSV-2) glycoprotein-G
CC (gG). They were isolated from a library of phage containing random 15-mer
CC peptide inserts that was screened with the murine monoclonal antibody
CC OlB90.E5 (E5). The peptides are not recognised by anti-gG2 negative sera
CC from patients with HSV-1 infection. The specification describes a
CC filamentous bacteriophage including in a portion of its major coat
CC protein sub-units multiple display of the peptide (or its analogues). The
CC peptides and the filamentous bacteriophage can be used in vaccine
CC compositions, which can be used to prevent HSV-2 infection. The peptides
CC and antibodies against them can be used to test for the presence of type-
CC specific HSV-2 gG2 antibodies in a fluid. This test can be used to
CC diagnose HSV-2 infection
XX
SQ Sequence 15 AA;

Query Match 31.6%; Score 31; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPD 10
| | | : | |
Db 5 DPPPPLHAPD 14

RESULT 33

AAW09376

ID AAW09376 standard; peptide; 16 AA.

XX

AC AAW09376;

XX

DT 17-JUN-1997 (first entry)

XX

DE Proline-rich antibacterial peptide from *Podisus maculiventris*.

XX

KW *Podisus maculiventris*; proline-rich; pathogenic; bacteria; bug;

KW Gram negative; plant treatment.

XX

OS *Podisus maculiventris*.

XX

PN FR2732345-A1.

XX

PD 04-OCT-1996.

XX

PF 03-APR-1995; 95FR-00004130.

XX

PR 03-APR-1995; 95FR-00004130.

XX

PA (RHON) RHONE POULENC AGROCHIMIE.

XX

PI Bulet P, Hoffman J, Hetru C, Tchernych S;

XX
 DR WPI; 1996-457711/46.
 XX
 PT Proline-rich antibacterial peptide(s) from *Podisus maculiventris* - esp.
 PT useful to protect plants against pathogenic bacteria, also for
 PT antibacterial therapy of animals.
 XX
 PS Claim 2; Page 14; 16pp; English.
 XX
 CC AAW09375-W09378 are specific examples of antibacterial peptides from the
 CC bug *Podisus maculiventris*. The proline-rich peptides have antibacterial
 CC activity against gram negative bacteria. They are useful for protecting
 CC plants against pathogenic bacteria, but could also be used for
 CC antibacterial therapy of animals, including humans. A generic peptide
 CC having the sequence VDKPDYRPRPX is also given in the specification, where
 CC X is a peptide comprising at least one PRP motif (see AAW17451)
 XX
 SQ Sequence 16 AA;

Query Match 31.6%; Score 31; DB 2; Length 16;
 Best Local Similarity 62.5%; Pred. No. 9.6e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13
 |:||| :|
 Db 1 VDKPDYRP 8

RESULT 34
 AAW09377
 ID AAW09377 standard; peptide; 16 AA.
 XX
 AC AAW09377;
 XX
 DT 17-JUN-1997 (first entry)
 XX
 DE Proline-rich antibacterial peptide from *Podisus maculiventris*.
 XX
 KW *Podisus maculiventris*; proline-rich; pathogenic; bacteria; bug;
 KW Gram negative; plant treatment.
 XX
 OS *Podisus maculiventris*.
 XX
 PN FR2732345-A1.
 XX
 PD 04-OCT-1996.
 XX
 PF 03-APR-1995; 95FR-00004130.
 XX
 PR 03-APR-1995; 95FR-00004130.
 XX
 PA (RHON) RHONE POULENC AGROCHIMIE.
 XX
 PI Bulet P, Hoffman J, Hetru C, Tchernych S;
 XX
 DR WPI; 1996-457711/46.
 XX

PT Proline-rich antibacterial peptide(s) from *Podisus maculiventris* - esp.
PT useful to protect plants against pathogenic bacteria, also for
PT antibacterial therapy of animals.
XX
PS Claim 2; Page 14; 16pp; English.
XX
CC AAW09375-W09378 are specific examples of antibacterial peptides from the
CC bug *Podisus maculiventris*. The proline-rich peptides have antibacterial
CC activity against gram negative bacteria. They are useful for protecting
CC plants against pathogenic bacteria, but could also be used for
CC antibacterial therapy of animals, including humans. A generic peptide
CC having the sequence VDKPDYRPRPX is also given in the specification, where
CC X is a peptide comprising at least one PRP motif (see AAW17451)
XX
SQ Sequence 16 AA;

Query Match 31.6%; Score 31; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 9.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13
|:|:|:|:|
Db 1 VDKPDYRP 8

RESULT 35

AAW12220

ID AAW12220 standard; peptide; 17 AA.

XX

AC AAW12220;

XX

DT 25-MAR-2003 (revised)

DT 25-MAR-1997 (first entry)

XX

DE Human acetylcholine receptor alpha chain amino acid 158-174.

XX

KW Tolerogenic conjugate; derivatisation; polymer; polyethylene glycol;

KW polyvinyl alcohol; immunotherapy; myasthenia gravis; autoimmune disease;

KW Grave's disease; allergy; antibody response.

XX

OS Synthetic.

XX

PN US5578496-A.

XX

PD 26-NOV-1996.

XX

PF 05-OCT-1994; 94US-00318200.

XX

PR 19-DEC-1991; 91US-00811050.

PR 20-OCT-1992; 92US-00965670.

XX

PA (BAYU) BAYLOR COLLEGE MEDICINE.

XX

PI Ashizawa T, Atassi MZ;

XX

DR WPI; 1997-020422/02.

XX

PT Diagnosing myasthenia gravis by detecting auto-antibodies to
PT acetyl:choline receptor - using set of peptide(s) derived from the
PT extracellular domain of the receptor, also therapeutic tolerogenic
PT peptide conjugates.

XX

PS Example 5; Col 41-42; 40pp; English.

XX

CC The peptides AAW12206-24 are derived from the human acetylcholine
CC receptor alpha-chain. This peptide corresponds to amino acids 158-174 of
CC the alpha-chain. The peptides are pref. derived from the extracellular
CC domain of the acetylcholine receptor. They are used in a method of
CC diagnosing an autoimmune disease, esp. myasthenia gravis, by recognising
CC autoantibodies associated with this disease. The peptides can also be
CC used to generate tolerogenic conjugates by derivatising the N-terminal
CC residue with a tolerogenic polymer, esp. monomethoxy-polyethylene glycol
CC or polyvinyl alcohol. The conjugates are esp. used for immunotherapy of
CC myasthenia gravis or other autoimmune disease such as Grave's disease, or
CC allergies, by suppressing antibody responses. (Updated on 25-MAR-2003 to
CC correct PF field.)

XX

SQ Sequence 17 AA;

Query Match 31.6%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 1e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 PDVEKPDLPF 14

|: ::||| |

Db 3 PESDQPDLSNF 13

RESULT 36

AAW09378

ID AAW09378 standard; peptide; 18 AA.

XX

AC AAW09378;

XX

DT 17-JUN-1997 (first entry)

XX

DE Proline-rich antibacterial peptide from *Podisus maculiventris*.

XX

KW *Podisus maculiventris*; proline-rich; pathogenic; bacteria; bug;

KW Gram negative; plant treatment.

XX

OS *Podisus maculiventris*.

XX

PN FR2732345-A1.

XX

PD 04-OCT-1996.

XX

PF 03-APR-1995; 95FR-00004130.

XX

PR 03-APR-1995; 95FR-00004130.

XX

PA (RHON) RHONE POULENC AGROCHIMIE.

XX

PI Bulet P, Hoffman J, Hetru C, Tchernych S;

XX
 DR WPI; 1996-457711/46.
 XX
 PT Proline-rich antibacterial peptide(s) from *Podisus maculiventris* - esp.
 PT useful to protect plants against pathogenic bacteria, also for
 PT antibacterial therapy of animals.
 XX
 PS Claim 2; Page 14; 16pp; English.
 XX
 CC AAW09375-W09378 are specific examples of antibacterial peptides from the
 CC bug *Podisus maculiventris*. The proline-rich peptides have antibacterial
 CC activity against gram negative bacteria. They are useful for protecting
 CC plants against pathogenic bacteria, but could also be used for
 CC antibacterial therapy of animals, including humans. A generic peptide
 CC having the sequence VDKPDYRPRPX is also given in the specification, where
 CC X is a peptide comprising at least one PRP motif (see AAW17451)
 XX
 SQ Sequence 18 AA;

Query Match 31.6%; Score 31; DB 2; Length 18;
 Best Local Similarity 62.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13
 |:| | | :|
 Db 1 VDKPDYRP 8

RESULT 37

AAR44563

ID AAR44563 standard; protein; 11 AA.

XX

AC AAR44563;

XX

DT 25-MAR-2003 (revised)

DT 26-MAY-1994 (first entry)

XX

DE Encoded by human Ews exon 10/Hum-Fli-1 exon 8 fusion.

XX

KW chromosomal translocation; chimeric; chimaeric; Ewing sarcoma; Ews gene;

KW malignant melanoma; hum-fli-1;

KW primitive peripheral neuroectodermal tumour; human chromosome 11;

KW human chromosome 22.

XX

OS *Homo sapiens*.

XX

FH Key Location/Qualifiers

FT Region 1. .5

FT /note= "encoded by 3'-end of Ews exon 10"

FT Region 6. .11

FT /note= "encoded by 5'-end of Hum-Fli-1 exon 8"

XX

PN W09323549-A2.

XX

PD 25-NOV-1993.

XX

PF 19-MAY-1993; 93WO-FR000494.

XX
 PR 20-MAY-1992; 92FR-00006123.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Aurias A, Delattre O, Desmaze C, Melot T, Peter M, Plougastel B;
 PI Thomas G, Zucman J;
 XX
 DR WPI; 1993-386580/48.
 DR N-PSDB; AAQ50676.
 XX
 PT New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence
 PT involved in chromosomal trans-location, also derived mRNA, probes, fusion
 PT proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma.
 XX
 PS Disclosure; Fig 14; 123pp; French.
 XX
 CC The intron-exon junctions of the human Ews gene and the Hum-Fli-1 gene
 CC have been sequenced (see AAQ50646 and AAQ50662, respectively). The
 CC different fusion products which could be formed by fusing exons from the
 CC two genes, as happens after specific chromosomal translocations, can be
 CC predicted. See AAR44558-R44565 for the amino acid sequences resulting
 CC from the different fusion events. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 31.1%; Score 30.5; DB 2; Length 11;
 Best Local Similarity 46.2%; Pred. No. 7.7e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

Qy 4 PDVEKPDLPFFQV 16
 ||: || |:|:
 Db 1 PDL---DLDPYQI 10

RESULT 38
 ABP55802
 ID ABP55802 standard; peptide; 9 AA.
 XX
 AC ABP55802;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE B15 class I sHLA molecule ligand related peptide #96.
 XX
 KW HLA ligand; human leukocyte antigen; predictive algorithm; database;
 KW MHC ligand; major histocompatibility complex; viral; bacterial; tumour.
 XX
 OS Synthetic.
 XX
 PN WO200269198-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 21-FEB-2002; 2002WO-US005298.
 XX

PR 21-FEB-2001; 2001US-0270357P.
PR 10-OCT-2001; 2001US-00974366.
PR 18-DEC-2001; 2001US-00022066.

XX

PA (HILD/) HILDEBRAND W H.
PA (PRIL/) PRILLIMAN K R.
PA (HICK/) HICKMAN H D.

XX

PI Hildebrand WH, Prilliman KR, Hickman HD;

XX

DR WPI; 2002-732755/79.

XX

PT Human leukocyte antigen ligand database assembled by producing HLA having
PT loaded ligands, isolating and sequencing loaded ligands to obtain HLA
PT ligand data and populating database in computer system with ligand data.

XX

PS Disclosure; Fig 5; 118pp; English.

XX

CC The present invention describes a human leukocyte antigen (HLA) (e.g.
CC soluble HLA) ligand database assembled by a process which involves
CC providing a computer system capable of storing HLA data as a database,
CC producing HLA having ligands loaded on it, isolating the loaded ligands
CC from HLA, sequencing the loaded ligands to obtain HLA ligand data, and
CC populating the database with HLA ligand data. Also described: (1)
CC accessing HLA (e.g. sHLA) data stored in a database; and (2) a computer
CC system for HLA (e.g. sHLA) ligand database. The database is populated
CC with HLA ligand sequences, motifs, extended motifs, submotifs, ligands
CC unique to infected cells, tumour specific ligands, as well as a
CC collection of current and future developed HLA ligand sequences. The
CC database which contains endogenously bound and loaded ligands facilitates
CC searching of viral, bacterial, tumour or human protein sequences for
CC ligands likely to bind a particular HLA class I or class II protein. The
CC database allows the user to screen an unknown peptide sequence for
CC potential matches with sHLA ligand discrete sequences or sHLA ligand
CC motifs of sequences. Due to the completeness and concentration of sHLA
CC obtained to date, better sequencing data of numerous endogenously loaded
CC HLA ligands is found in the sHLA ligand database, and by comparison of
CC such ligands to each other and to the genomic sequence, better motifs are
CC also found in the sHLA ligand database. ABP55692 to ABP55912 represent
CC amino acid sequences used in the exemplification of the present invention

XX

SQ Sequence 9 AA;

Query Match 30.6%; Score 30; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQPPDVE 7

| |||::

Db 2 DPPPDMZ 8

RESULT 39

ABG96846

ID ABG96846 standard; peptide; 9 AA.

XX

AC ABG96846;

XX
DT 16-DEC-2002 (first entry)
XX
DE Human leukocyte antigen (HLA) B15 ligand #171.
XX
KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;
KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
KW viral infection; cancer; autoimmune disease; vaccine development; MHC;
KW major histocompatibility complex; diagnostic development;
KW HLA class I polymorphism; HLA-B15 allotype; ligand.
XX
OS Homo sapiens.
XX
PN WO200262846-A2.
XX
PD 15-AUG-2002.
XX
PF 18-DEC-2001; 2001WO-US049744.
XX
PR 18-DEC-2000; 2000US-0256409P.
PR 18-DEC-2000; 2000US-0256410P.
PR 10-OCT-2001; 2001US-00974366.
XX
PA (HILD/) HILDEBRAND W H.
PA (PRIL/) PRILLIMAN K R.
XX
PI Hildebrand WH, Prilliman KR;
XX
DR WPI; 2002-698563/75.
XX
PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
PT studies of peptide loading for characterizing human immune responses
PT involves using HLA allelic cDNA or genomic DNA as starting material.
XX
PS Disclosure; Page 178; 300pp; English.
XX
CC The invention describes a method of producing soluble human leukocyte
CC antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA
CC allelic DNA by PCR using a locus specific primer to produce truncated a
CC PCR product (PI), inserting PI into mammalian expression vector;
CC electroporating the plasmid into a host cell; inoculating the cell pharm
CC with the host cell such that cell pharm produces sHLA. A multimeric HLA
CC complex (I) is useful for testing functionality of peptide ligands bound
CC by at least two soluble HLA molecules. (I) can be tested for its ability
CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
CC responses in humans. (I) is useful for studying T cell responses to
CC pathological conditions such as viral infections and cancer, and for
CC modulating the human immune system to induce tolerance in autoimmune
CC diseases. The individual secreted major histocompatibility complex (MHC)
CC molecules produced are useful for studies of peptide loading (i.e., in
CC vaccine development) and to the development of diagnostics. With the
CC secreted MHC molecules, naturally loaded peptides can be eluted from the
CC MHC molecule and characterised. The secreted MHC molecules allow the
CC assessment of structural and functional impact of HLA class I
CC polymorphism. The molecules are also useful to generate ligands and hence
CC ligand maps from the peptide pools extracted from series of distinct yet
CC related class I HLA-B15 allotypes; compare the different ligand maps to

CC identify potentially shared elements; and characterise the elements
CC identified to positively or negatively validate the occurrence of
CC overlapping ligands. The truncated version of (MHC) can be produced in
CC mammalian or insect/bacterial cells such that milligram or greater
CC quantities of an individual class I or class II molecule can be obtained.
CC This sequence represents a HLA (human leukocyte antigen) peptide ligand
XX
SQ Sequence 9 AA;

Query Match 30.6%; Score 30; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQPPDVE 7
| |||::
Db 2 DPPPDMZ 8

RESULT 40
ABG96954

ID ABG96954 standard; peptide; 9 AA.

XX

AC ABG96954;

XX

DT 16-DEC-2002 (first entry)

XX

DE Human leukocyte antigen (HLA) B15 ligand #282.

XX

KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;

KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;

KW viral infection; cancer; autoimmune disease; vaccine development; MHC;

KW major histocompatibility complex; diagnostic development;

KW HLA class I polymorphism; HLA-B15 allotype; ligand.

XX

OS Homo sapiens.

XX

PN WO200262846-A2.

XX

PD 15-AUG-2002.

XX

PF 18-DEC-2001; 2001WO-US049744.

XX

PR 18-DEC-2000; 2000US-0256409P.

PR 18-DEC-2000; 2000US-0256410P.

PR 10-OCT-2001; 2001US-00974366.

XX

PA (HILD/) HILDEBRAND W H.

PA (PRIL/) PRILLIMAN K R.

XX

PI Hildebrand WH, Prilliman KR;

XX

DR WPI; 2002-698563/75.

XX

PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful for

PT studies of peptide loading for characterizing human immune responses

PT involves using HLA allelic cDNA or genomic DNA as starting material.

XX

PS Disclosure; Page 181; 300pp; English.

XX

CC The invention describes a method of producing soluble human leukocyte
CC antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA
CC allelic DNA by PCR using a locus specific primer to produce truncated a
CC PCR product (PI), inserting PI into mammalian expression vector;
CC electroporating the plasmid into a host cell; inoculating the cell pharm
CC with the host cell such that cell pharm produces sHLA. A multimeric HLA
CC complex (I) is useful for testing functionality of peptide ligands bound
CC by at least two soluble HLA molecules. (I) can be tested for its ability
CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
CC responses in humans. (I) is useful for studying T cell responses to
CC pathological conditions such as viral infections and cancer, and for
CC modulating the human immune system to induce tolerance in autoimmune
CC diseases. The individual secreted major histocompatibility complex (MHC)
CC molecules produced are useful for studies of peptide loading (i.e., in
CC vaccine development) and to the development of diagnostics. With the
CC secreted MHC molecules, naturally loaded peptides can be eluted from the
CC MHC molecule and characterised. The secreted MHC molecules allow the
CC assessment of structural and functional impact of HLA class I
CC polymorphism. The molecules are also useful to generate ligands and hence
CC ligand maps from the peptide pools extracted from series of distinct yet
CC related class I HLA-B15 allotypes; compare the different ligand maps to
CC identify potentially shared elements; and characterise the elements
CC identified to positively or negatively validate the occurrence of
CC overlapping ligands. The truncated version of (MHC) can be produced in
CC mammalian or insect/bacterial cells such that milligram or greater
CC quantities of an individual class I or class II molecule can be obtained.
CC This sequence represents a HLA (human leukocyte antigen) peptide ligand

XX

SQ Sequence 9 AA;

Query Match 30.6%; Score 30; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQPPDVE 7

| |||::

Db 2 DPPPDMZ 8

RESULT 41

ABG96698

ID ABG96698 standard; peptide; 9 AA.

XX

AC ABG96698;

XX

DT 16-DEC-2002 (first entry)

XX

DE Human leukocyte antigen (HLA) B15 ligand #121.

XX

KW Soluble human leukocyte antigen; HLA; sHLA; cell pharm;

KW multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;

KW viral infection; cancer; autoimmune disease; vaccine development; MHC;

KW major histocompatibility complex; diagnostic development;

KW HLA class I polymorphism; HLA-B15 allotype; ligand.

XX

OS Homo sapiens.
 XX
 PN WO200262846-A2.
 XX
 PD 15-AUG-2002.
 XX
 PF 18-DEC-2001; 2001WO-US049744.
 XX
 PR 18-DEC-2000; 2000US-0256409P.
 PR 18-DEC-2000; 2000US-0256410P.
 PR 10-OCT-2001; 2001US-00974366.
 XX
 PA (HILD/) HILDEBRAND W H.
 PA (PRIL/) PRILLIMAN K R.
 XX
 PI Hildebrand WH, Prilliman KR;
 XX
 DR WPI; 2002-698563/75.
 XX
 PT Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
 PT studies of peptide loading for characterizing human immune responses
 PT involves using HLA allelic cDNA or genomic DNA as starting material.
 XX
 PS Disclosure; Fig 26; 300pp; English.
 XX
 CC The invention describes a method of producing soluble human leukocyte
 CC antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA
 CC allelic DNA by PCR using a locus specific primer to produce truncated a
 CC PCR product (PI), inserting PI into mammalian expression vector;
 CC electroporating the plasmid into a host cell; inoculating the cell pharm
 CC with the host cell such that cell pharm produces sHLA. A multimeric HLA
 CC complex (I) is useful for testing functionality of peptide ligands bound
 CC by at least two soluble HLA molecules. (I) can be tested for its ability
 CC to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune
 CC responses in humans. (I) is useful for studying T cell responses to
 CC pathological conditions such as viral infections and cancer, and for
 CC modulating the human immune system to induce tolerance in autoimmune
 CC diseases. The individual secreted major histocompatibility complex (MHC)
 CC molecules produced are useful for studies of peptide loading (i.e., in
 CC vaccine development) and to the development of diagnostics. With the
 CC secreted MHC molecules, naturally loaded peptides can be eluted from the
 CC MHC molecule and characterised. The secreted MHC molecules allow the
 CC assessment of structural and functional impact of HLA class I
 CC polymorphism. The molecules are also useful to generate ligands and hence
 CC ligand maps from the peptide pools extracted from series of distinct yet
 CC related class I HLA-B15 allotypes; compare the different ligand maps to
 CC identify potentially shared elements; and characterise the elements
 CC identified to positively or negatively validate the occurrence of
 CC overlapping ligands. The truncated version of (MHC) can be produced in
 CC mammalian or insect/bacterial cells such that milligram or greater
 CC quantities of an individual class I or class II molecule can be obtained.
 CC This sequence represents a HLA (human leukocyte antigen) peptide ligand
 XX
 SQ Sequence 9 AA;

Query Match 30.6%; Score 30; DB 5; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQPPDVE 7
| |||::
Db 2 DPPPDMZ 8

RESULT 42

ADC35017

ID ADC35017 standard; peptide; 11 AA.

XX

AC ADC35017;

XX

DT 18-DEC-2003 (first entry)

XX

DE Rho-like protein C-terminal peptide #14.

XX

KW protein transduction domain; PTD; cell-penetrating capacity; C-terminus;

KW Ras-like GTPase; Ras-like GTPase inhibition;

KW leukaemic cell migration inhibition; leukaemia; Rho-like protein.

XX

OS Unidentified.

XX

PN WO2003042239-A1.

XX

PD 22-MAY-2003.

XX

PF 11-NOV-2002; 2002WO-NL000722.

XX

PR 12-NOV-2001; 2001EP-00204305.

XX

PA (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.

XX

PI Ten Klooster JP, Van Hennik PB, Voermans C, Hordijk PL;

XX

DR WPI; 2003-568944/53.

XX

PT New protein transduction domain peptides having cell-penetrating

PT capacity, are useful for inhibiting cellular functions mediated by the

PT Ras-like GTPase in eukaryotic cells, and for inhibiting leukemic cell

PT migration.

XX

PS Disclosure; Page 14; 46pp; English.

XX

CC The invention comprises amino acid sequences corresponding to a protein

CC transduction domain (PTD) which has a cell-penetrating capacity and an

CC amino acid sequence corresponding to a variable part of the C-terminus of

CC a Ras-like GTPase having Ras-like GTPase signalling capacity. The

CC peptides of the invention are useful for inhibiting cellular functions

CC mediated by the Ras-like GTPase in eukaryotic cells - particularly

CC mammalian cells, and for inhibiting leukaemic cell migration. The present

CC amino acid sequence represents a C-terminal sequence from a Rho-like

CC protein.

XX

SQ Sequence 11 AA;

Query Match 30.6%; Score 30; DB 7; Length 11;

Best Local Similarity 71.4%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPDVEKP 9
|||:
Db 2 PPPVKKP 8

RESULT 43

ABB97741

ID ABB97741 standard; peptide; 13 AA.

XX

AC ABB97741;

XX

DT 11-JUL-2002 (first entry)

XX

DE Human procathepsin W epitope peptide #121.

XX

KW Human; procathepsin W; cathepsin W; monoclonal antibody; epitope.

XX

OS Homo sapiens.

XX

PN WO200226831-A1.

XX

PD 04-APR-2002.

XX

PF 09-JUL-2001; 2001WO-EP007877.

XX

PR 29-SEP-2000; 2000DE-01048727.

XX

PA (LABS-) LABSOFT DIAGNOSTICS AG.

XX

PI Weber E;

XX

DR WPI; 2002-330095/36.

XX

PT New hybridoma cell lines that produces antibodies specific for human

PT cathepsin W, useful e.g. for diagnosis, therapy and drug targeting.

XX

PS Disclosure; Fig 1; 23pp; German.

XX

CC The present invention relates to hybridoma cell lines that produce

CC monoclonal antibodies directed against a defined epitope of human

CC (pro)cathepsin W, which are produced by fusing myeloma cells with spleen

CC cells from an animal that has been immunised with recombinant

CC procathepsin W. The antibodies produced are useful for analysis,

CC diagnosis (detection of human (pro)cathepsin W), purification of

CC (pro)cathepsin W (also for clarifying processing of the precursor and

CC functional significance of the mature protein), for drug targeting and

CC for therapeutic use. The present sequence is an epitope of human

CC procathepsin W

XX

SQ Sequence 13 AA;

Query Match 30.6%; Score 30; DB 5; Length 13;

Best Local Similarity 57.1%; Pred. No. 1.1e+03;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 7 EKPDLQP 13
:|||::|
Db 1 QKPDMPK 7

RESULT 44

AAG88540

ID AAG88540 standard; peptide; 15 AA.

XX

AC AAG88540;

XX

DT 11-SEP-2001 (first entry)

XX

DE HER2/NEU DR supermotif binding peptide exemplary sequence #126.

XX

KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;

KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;

KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200141787-A1.

XX

PD 14-JUN-2001.

XX

PF 11-DEC-2000; 2000WO-US033591.

XX

PR 10-DEC-1999; 99US-00458299.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;

PI Keogh E;

XX

DR WPI; 2001-374995/39.

XX

PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
PT cellular immune responses for the prevention and treatment of cancer.

XX

PS Disclosure; Page 170; 199pp; English.

XX

CC The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and
CC immunostimulant activities, and can be used in vaccines. (I), (II) and
CC (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample from a patient and

CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention

XX

SQ Sequence 15 AA;

Query Match 30.6%; Score 30; DB 4; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLP 13

| | :||::|

Db 1 PEYVNQPDVRP 11

RESULT 45

ABR30154

ID ABR30154 standard; peptide; 15 AA.

XX

AC ABR30154;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human cancer-related protein 74P3B3 HLA peptide #2998.

XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX

OS Homo sapiens.

XX

PN WO200283921-A2.

XX

PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US011654.

XX

PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX

DR WPI; 2003-075555/07.

XX

PT New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

XX

PS Claim 13; Page 469; 1021pp; English.

XX

CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention

XX

SQ Sequence 15 AA;

Query Match 30.6%; Score 30; DB 6; Length 15;
Best Local Similarity 30.8%; Pred. No. 1.3e+03;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPFQ 15

|| ::: |:|::

Db 2 PPPIKQCSLEPWR 14

RESULT 46

ADE70385

ID ADE70385 standard; peptide; 15 AA.

XX

AC ADE70385;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human 161P2F10B protein-related peptide 4390.

XX

KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.

XX

OS Homo sapiens.

XX

PN WO2003040340-A2.

XX

PD 15-MAY-2003.

XX

PF 07-NOV-2002; 2002WO-US036002.

XX

PR 07-NOV-2001; 2001US-00005480.

PR 31-JAN-2002; 2002US-00062109.

XX

PA (AGEN-) AGENSYS INC.

XX

PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;

PI Morrison RK, Challita-Eid PM;

XX
 DR WPI; 2003-441560/41.
 XX
 PT A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 PS Claim 13; Page 178; 135pp; English.
 XX
 CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 30.6%; Score 30; DB 7; Length 15;
 Best Local Similarity 38.5%; Pred. No. 1.3e+03;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPFFQ 15
 | || ::||:
 Db 2 PSFKEKTEVEPFE 14

RESULT 47

ADE70790

ID ADE70790 standard; peptide; 15 AA.

XX

AC ADE70790;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human 161P2F10B protein-related peptide 4795.

XX

KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.

XX

OS Homo sapiens.

XX

PN WO2003040340-A2.

XX

PD 15-MAY-2003.

XX

PF 07-NOV-2002; 2002WO-US036002.

XX

PR 07-NOV-2001; 2001US-00005480.

PR 31-JAN-2002; 2002US-00062109.

XX

PA (AGEN-) AGENSYS INC.

XX
 PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX
 DR WPI; 2003-441560/41.
 XX
 PT A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 PS Claim 13; Page 182; 135pp; English.
 XX
 CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 30.6%; Score 30; DB 7; Length 15;
 Best Local Similarity 38.5%; Pred. No. 1.3e+03;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 PPDVEKPDQLQPFQ 15
 | || ::||:
 Db 2 PSFKEKTEVEPF 14

RESULT 48
 ADE70192

ID ADE70192 standard; peptide; 15 AA.
 XX
 AC ADE70192;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human 161P2F10B protein-related peptide 4197.
 XX
 KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040340-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 07-NOV-2002; 2002WO-US036002.
 XX
 PR 07-NOV-2001; 2001US-00005480.

PR 31-JAN-2002; 2002US-00062109.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;
 PI Morrison RK, Challita-Eid PM;
 XX
 DR WPI; 2003-441560/41.
 XX
 PT A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX
 PS Claim 13; Page 177; 135pp; English.
 XX
 CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC be useful for gene therapy or the development of a vaccine. The
 CC composition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 30.6%; Score 30; DB 7; Length 15;
 Best Local Similarity 38.5%; Pred. No. 1.3e+03;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPFQ 15
 | ||::||:
 Db 2 PSFKEKTEVEPFE 14

RESULT 49
 AAU01833
 ID AAU01833 standard; peptide; 17 AA.
 XX
 AC AAU01833;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Wheat Gliadin peptide J.
 XX
 KW Wheat; A-gliadin; peptide J; coeliac disease; gluten intolerance;
 KW T-cell binding; antagonist; transglutaminase; transgenic plant.
 XX
 OS Triticum aestivum.
 XX
 PN WO200125793-A2.
 XX
 PD 12-APR-2001.

XX
PF 02-OCT-2000; 2000WO-GB003760.
XX
PR 01-OCT-1999; 99GB-00023306.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Anderson RP, Hill AVS, Jewell DP;
XX
DR WPI; 2001-300179/31.
XX
PT Diagnosing coeliac disease or susceptibility to the disease in an
PT individual, by detecting in vitro or in vivo T cells which bind
PT immunodominant T cell epitope obtained from naturally occurring homolog
PT of gliadin.
XX
PS Example 8; Fig 14; 107pp; English.
XX
CC The sequence represents wheat Gliadin peptide J, corresponding to A-
CC gliadin 57-73 and containing a natural polymorphism. The peptides of the
CC invention are used to test mammalian (preferably human) susceptibility to
CC coeliac disease (gluten intolerance). The peptides are contacted with a
CC blood sample and T cell recognition measured, a positive T-cell
CC recognition indicating a susceptibility to coeliac disease. The peptides
CC are useful for inducing tolerance in an individual and antagonists to the
CC peptides are useful for treating or preventing coeliac disease in an
CC individual and for producing an antibody specific to them or a wild-type
CC sequence. A mutant gliadin protein (or its fragment of 15 amino acids in
CC length) whose wild-type sequence can be modified by transglutaminase to a
CC sequence that comprises the epitope, but which has been modified in such
CC a way that it does not contain sequence which can be modified by
CC transglutaminase to a sequence that comprise the epitope is useful for
CC decreasing the ability of gliadin protein to cause Coeliac disease.
CC Nucleic acids encoding proteins antagonistic to the T-cell binding of the
CC epitopes are useful for obtaining a transgenic plant cell or seed and for
CC the production of a protein. The resultant crop plant is useful for
CC obtaining a product of a wheat plant, especially grain, which is
CC optionally processed into flour or another grain product. Food comprising
CC the antagonistic protein is useful instead of a wild-type gliadin
XX
SQ Sequence 17 AA;

Query Match 30.6%; Score 30; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPQ 13
|| : | ||
Db 7 PPQLPYPQTQP 17

RESULT 50
AAU01822
ID AAU01822 standard; peptide; 17 AA.
XX
AC AAU01822;
XX

DT 07-SEP-2001 (first entry)
 XX
 DE Wheat Gliadin peptide O.
 XX
 KW Wheat; A-gliadin; peptide O; coeliac disease; gluten intolerance;
 KW T-cell binding; antagonist; transglutaminase; transgenic plant.
 XX
 OS Triticum aestivum.
 XX
 PN WO200125793-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 02-OCT-2000; 2000WO-GB003760.
 XX
 PR 01-OCT-1999; 99GB-00023306.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 XX
 PI Anderson RP, Hill AVS, Jewell DP;
 XX
 DR WPI; 2001-300179/31.
 XX
 PT Diagnosing coeliac disease or susceptibility to the disease in an
 PT individual, by detecting in vitro or in vivo T cells which bind
 PT immunodominant T cell epitope obtained from naturally occurring homolog
 PT of gliadin.
 XX
 PS Example 8; Fig 14; 107pp; English.
 XX
 CC The sequence represents wheat Gliadin peptide O, corresponding to A-
 CC gliadin 57-73 and containing a natural polymorphism. The peptides of the
 CC invention are used to test mammalian (preferably human) susceptibility to
 CC coeliac disease (gluten intolerance). The peptides are contacted with a
 CC blood sample and T cell recognition measured, a positive T-cell
 CC recognition indicating a susceptibility to coeliac disease. The peptides
 CC are useful for inducing tolerance in an individual and antagonists to the
 CC peptides are useful for treating or preventing coeliac disease in an
 CC individual and for producing an antibody specific to them or a wild-type
 CC sequence. A mutant gliadin protein (or its fragment of 15 amino acids in
 CC length) whose wild-type sequence can be modified by transglutaminase to a
 CC sequence that comprises the epitope, but which has been modified in such
 CC a way that it does not contain sequence which can be modified by
 CC transglutaminase to a sequence that comprise the epitope is useful for
 CC decreasing the ability of gliadin protein to cause Coeliac disease.
 CC Nucleic acids encoding proteins antagonistic to the T-cell binding of the
 CC epitopes are useful for obtaining a transgenic plant cell or seed and for
 CC the production of a protein. The resultant crop plant is useful for
 CC obtaining a product of a wheat plant, especially grain, which is
 CC optionally processed into flour or another grain product. Food comprising
 CC the antagonistic protein is useful instead of a wild-type gliadin
 XX
 SQ Sequence 17 AA;

Query Match 30.6%; Score 30; DB 4; Length 17;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLP 13
|| : | ||
Db 7 PPQLPYPTQP 17

Search completed: July 4, 2004, 04:40:39
Job time : 46.1791 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:37:26 ; Search time 11.2836 Seconds
(without alignments)
82.356 Million cell updates/sec

Title: US-09-641-802-3
Perfect score: 98
Sequence: 1 DQPPDVEKPDLPFQVQS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121837

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%				
		Query				
Result	No.	Score	Match	Length	ID	Description
1	98	100.0	18	4	US-09-641-803-3	Sequence 3, Appli
2	33	33.7	14	2	US-07-963-538B-10	Sequence 10, Appl
3	33	33.7	18	2	US-08-769-745-20	Sequence 20, Appl
4	32	32.7	18	3	US-08-602-999A-305	Sequence 305, App
5	32	32.7	18	4	US-09-500-124-305	Sequence 305, App
6	31	31.6	17	1	US-08-318-200-21	Sequence 21, Appl
7	31	31.6	18	1	US-08-336-618-11	Sequence 11, Appl
8	30.5	31.1	11	2	US-08-343-443B-74	Sequence 74, Appl
9	30.5	31.1	11	2	US-08-343-443B-94	Sequence 94, Appl
10	29	29.6	15	4	US-09-914-259-70	Sequence 70, Appl
11	29	29.6	17	1	US-08-144-121-12	Sequence 12, Appl

12	29	29.6	17	2	US-08-735-893-12	Sequence 12, Appl
13	29	29.6	18	3	US-09-461-697-200	Sequence 200, App
14	28	28.6	12	1	US-08-190-788A-43	Sequence 43, Appl
15	28	28.6	12	1	US-08-190-788A-52	Sequence 52, Appl
16	28	28.6	12	1	US-08-190-788A-284	Sequence 284, App
17	28	28.6	12	1	US-08-383-474B-48	Sequence 48, Appl
18	28	28.6	12	1	US-08-383-474B-57	Sequence 57, Appl
19	28	28.6	12	1	US-08-383-474B-285	Sequence 285, App
20	28	28.6	12	1	US-08-465-391A-43	Sequence 43, Appl
21	28	28.6	12	1	US-08-465-391A-52	Sequence 52, Appl
22	28	28.6	12	1	US-08-465-391A-284	Sequence 284, App
23	28	28.6	12	2	US-08-464-538B-43	Sequence 43, Appl
24	28	28.6	12	2	US-08-464-538B-52	Sequence 52, Appl
25	28	28.6	12	2	US-08-464-538B-283	Sequence 283, App
26	28	28.6	12	2	US-08-463-076E-87	Sequence 87, Appl
27	28	28.6	12	2	US-08-463-076E-96	Sequence 96, Appl
28	28	28.6	12	2	US-08-463-076E-357	Sequence 357, App
29	28	28.6	12	4	US-09-428-082B-673	Sequence 673, App
30	28	28.6	12	4	US-09-428-082B-683	Sequence 683, App
31	28	28.6	12	4	US-09-428-082B-958	Sequence 958, App
32	28	28.6	13	2	US-08-347-335A-13	Sequence 13, Appl
33	28	28.6	15	1	US-08-467-083-53	Sequence 53, Appl
34	28	28.6	15	1	US-08-414-417B-53	Sequence 53, Appl
35	28	28.6	15	2	US-08-486-348A-53	Sequence 53, Appl
36	28	28.6	15	2	US-08-468-545B-53	Sequence 53, Appl
37	28	28.6	15	3	US-08-466-680B-53	Sequence 53, Appl
38	28	28.6	15	4	US-09-354-533-53	Sequence 53, Appl
39	28	28.6	16	1	US-08-190-788A-170	Sequence 170, App
40	28	28.6	16	1	US-08-383-474B-173	Sequence 173, App
41	28	28.6	16	1	US-08-465-391A-170	Sequence 170, App
42	28	28.6	16	2	US-08-464-538B-170	Sequence 170, App
43	28	28.6	16	2	US-08-463-076E-223	Sequence 223, App
44	28	28.6	16	4	US-09-428-082B-786	Sequence 786, App
45	28	28.6	17	1	US-08-190-788A-169	Sequence 169, App
46	28	28.6	17	1	US-08-190-788A-230	Sequence 230, App
47	28	28.6	17	1	US-08-190-788A-233	Sequence 233, App
48	28	28.6	17	1	US-08-190-788A-234	Sequence 234, App
49	28	28.6	17	1	US-08-383-474B-172	Sequence 172, App
50	28	28.6	17	1	US-08-383-474B-233	Sequence 233, App
51	28	28.6	17	1	US-08-383-474B-236	Sequence 236, App
52	28	28.6	17	1	US-08-383-474B-237	Sequence 237, App
53	28	28.6	17	1	US-08-465-391A-169	Sequence 169, App
54	28	28.6	17	1	US-08-465-391A-230	Sequence 230, App
55	28	28.6	17	1	US-08-465-391A-233	Sequence 233, App
56	28	28.6	17	1	US-08-465-391A-234	Sequence 234, App
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58	28	28.6	17	2	US-08-464-538B-230	Sequence 230, App
59	28	28.6	17	2	US-08-464-538B-233	Sequence 233, App
60	28	28.6	17	2	US-08-464-538B-234	Sequence 234, App
61	28	28.6	17	2	US-08-463-076E-222	Sequence 222, App
62	28	28.6	17	2	US-08-463-076E-284	Sequence 284, App
63	28	28.6	17	2	US-08-463-076E-287	Sequence 287, App
64	28	28.6	17	2	US-08-463-076E-288	Sequence 288, App
65	28	28.6	17	3	US-08-602-999A-338	Sequence 338, App
66	28	28.6	17	4	US-09-500-124-338	Sequence 338, App
67	28	28.6	17	4	US-09-428-082B-785	Sequence 785, App
68	28	28.6	17	4	US-09-428-082B-844	Sequence 844, App

69	28	28.6	17	4	US-09-428-082B-847	Sequence 847, App
70	28	28.6	17	4	US-09-428-082B-848	Sequence 848, App
71	27	27.6	8	1	US-07-923-724-48	Sequence 48, Appl
72	27	27.6	8	2	US-08-609-426A-48	Sequence 48, Appl
73	27	27.6	8	2	US-08-374-652C-38	Sequence 38, Appl
74	27	27.6	9	2	US-08-146-028-431	Sequence 431, App
75	27	27.6	9	2	US-08-146-028-432	Sequence 432, App
76	27	27.6	9	2	US-08-146-028-433	Sequence 433, App
77	27	27.6	9	3	US-08-723-425A-431	Sequence 431, App
78	27	27.6	9	3	US-08-723-425A-432	Sequence 432, App
79	27	27.6	9	3	US-08-723-425A-433	Sequence 433, App
80	27	27.6	9	3	US-09-112-206-431	Sequence 431, App
81	27	27.6	9	3	US-09-112-206-432	Sequence 432, App
82	27	27.6	9	3	US-09-112-206-433	Sequence 433, App
83	27	27.6	9	3	US-09-518-046-148	Sequence 148, App
84	27	27.6	9	4	US-09-790-497A-379	Sequence 379, App
85	27	27.6	9	4	US-09-790-497A-380	Sequence 380, App
86	27	27.6	9	4	US-09-790-497A-381	Sequence 381, App
87	27	27.6	9	4	US-09-790-497A-564	Sequence 564, App
88	27	27.6	9	4	US-09-790-497A-565	Sequence 565, App
89	27	27.6	9	4	US-09-790-497A-566	Sequence 566, App
90	27	27.6	9	4	US-09-576-824A-379	Sequence 379, App
91	27	27.6	9	4	US-09-576-824A-380	Sequence 380, App
92	27	27.6	9	4	US-09-576-824A-381	Sequence 381, App
93	27	27.6	10	3	US-08-762-428A-1	Sequence 1, Appli
94	27	27.6	11	4	US-09-576-824A-564	Sequence 564, App
95	27	27.6	11	4	US-09-576-824A-565	Sequence 565, App
96	27	27.6	11	4	US-09-576-824A-566	Sequence 566, App
97	27	27.6	11	4	US-09-576-824A-567	Sequence 567, App
98	27	27.6	12	1	US-08-190-788A-162	Sequence 162, App
99	27	27.6	12	1	US-08-383-474B-165	Sequence 165, App
100	27	27.6	12	1	US-08-465-391A-162	Sequence 162, App

ALIGNMENTS

RESULT 1

US-09-641-803-3

; Sequence 3, Application US/09641803

; Patent No. 6500798

; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND

; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS

; FILE REFERENCE: 265.00220101

; CURRENT APPLICATION NUMBER: US/09/641,803

; CURRENT FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: 60/149,310

; PRIOR FILING DATE: 1999-08-17

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-3

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPFQVQS 18
| | | | | | | | | | | | | | | |
Db 1 DQPPDVEKPDLPFQVQS 18

RESULT 2

US-07-963-538B-10

; Sequence 10, Application US/07963538B

; Patent No. 5851983

; GENERAL INFORMATION:

; APPLICANT: SUGIYAMA, TAKASHI

; APPLICANT: KAMIMURA, TAKASHI

; APPLICANT: MASUDA, KENICHI

; APPLICANT: OKADA, MASAHIRO

; APPLICANT: OHTSUKA, EIKO

; APPLICANT: IMAIZUMI, ATSUSHI

; APPLICANT: WATANABE, KUNIHITO

; APPLICANT: SUGA, TETSUYA

; APPLICANT: MATSUMOTO, YOHICHI

; APPLICANT: TAKEUCHI, AKIKO

; TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND

; TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE

; TITLE OF INVENTION: TECHNOLOGY

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: COOLEY GODWARD LLP

; STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR

; CITY: PALO ALTO

; STATE: CA

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/963,538B

; FILING DATE: 20-OCT-1992

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/843,359

; FILING DATE: 25-FEB-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/408,483

; FILING DATE: 22-AUG-1989

; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: JP 4-212399
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-212398
; FILING DATE: 17-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-355553
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 62-330219
; FILING DATE: 28-DEC-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY PH.D., RICHARD L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: TEJN-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5070
; TELEFAX: 415-857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-963-538B-10

```

```

Query Match          33.7%; Score 33; DB 2; Length 14;
Best Local Similarity 53.8%; Pred. No. 53;
Matches      7; Conservative      0; Mismatches      6; Indels      0; Gaps      0;

```

```

Qy      1 DQPPDVEKPDLP 13
        | ||| | |
Db      1 DDPPTVELQGLVP 13

```

```

RESULT 3
US-08-769-745-20
; Sequence 20, Application US/08769745
; Patent No. 5955259
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd C.
; APPLICANT: Levitan, Irwin B.
; APPLICANT: Brandeis University
; TITLE OF INVENTION: Mechanism for the Regulation of Ion
; TITLE OF INVENTION: Channel Activity
; FILE REFERENCE: BRU96-02
; CURRENT APPLICATION NUMBER: US/08/769,745
; CURRENT FILING DATE: 1996-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Rat
US-08-769-745-20

```

Query Match 33.7%; Score 33; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLP 13
|||: | | |
Db 6 QPPESSPPPLP 17

RESULT 4

US-08-602-999A-305

; Sequence 305, Application US/08602999A

; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A

; FILING DATE: 16-FEB-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 305:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-602-999A-305

Query Match 32.7%; Score 32; DB 3; Length 18;

Best Local Similarity 43.8%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLPFFQVQ 17
||| | || |
Db 3 QPPYFPPPPYQPIYPQ 18

RESULT 5

US-09-500-124-305

; Sequence 305, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-305

Query Match 32.7%; Score 32; DB 4; Length 18;
Best Local Similarity 43.8%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLPFFQVQ 17
||| | || |
Db 3 QPPYFPPPPYQPIYPQ 18

RESULT 6

US-08-318-200-21

; Sequence 21, Application US/08318200

; Patent No. 5578496

; GENERAL INFORMATION:

; APPLICANT: Atassi, M. Z.

; APPLICANT: Ashizawa, T.

; TITLE OF INVENTION: N-TERMINAL PVA- OR PEG-CONJUGATED

; TITLE OF INVENTION: PEPTIDES FOR EPITOPE-SPECIFIC IMMUNOSUPPRESSION

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: PO Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/318,200

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/965,670

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: McDaniel, C. Steven

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713-787-1400

; TELEFAX: 713-789-2679

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-318-200-21

Query Match 31.6%; Score 31; DB 1; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 PDVEKPDLPF 14

Db |: ::||| |
 3 PESDQPDLSNF 13

RESULT 7

US-08-336-618-11

; Sequence 11, Application US/08336618

; Patent No. 5763590

; GENERAL INFORMATION:

; APPLICANT: Peattie, Debra A.

; APPLICANT: Harding, Matthew W.

; APPLICANT: Livingston, David J.

; TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING

; TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN

; TITLE OF INVENTION: cDNA

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/336,618

; FILING DATE: 09-NOV-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/963,325

; FILING DATE: 16-OCT-1992

; APPLICATION NUMBER: US 07/777,752

; FILING DATE: 11-OCT-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/

; FILING DATE: 09-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 32,227

; REFERENCE/DOCKET NUMBER: VPI91-06A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-336-618-11

Query Match 31.6%; Score 31; DB 1; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPD 10
||| | | |
Db 7 DQPADAEMRD 16

RESULT 8

US-08-343-443B-74

; Sequence 74, Application US/08343443B

; Patent No. 5968734

; GENERAL INFORMATION:

; APPLICANT: Aurias, Alain

; APPLICANT: Delattre, Olivier

; APPLICANT: Desmaze, Chantal

; APPLICANT: Melot, Thomas

; APPLICANT: Peter, Martine

; APPLICANT: Ploougastel, Beatrice

; APPLICANT: Thomas, Gilles

; APPLICANT: Zucman, Jessica

; TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF

; TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL

; TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF

CANCEROUS

; TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM
SAID

; TITLE OF INVENTION: TRANSLOCATIONS

; NUMBER OF SEQUENCES: 129

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Weiser & Associates

; STREET: 230 South Fifteenth Street

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: AEDIT 1.0 DOS text editor

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/343,443B

; FILING DATE: 18-NOV-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR93/00494

; FILING DATE: 19-MAY-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 92/06123

; FILING DATE: 20-MAY-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Weiser, Gerard J.

; REGISTRATION NUMBER: 19,763

; REFERENCE/DOCKET NUMBER: 989.6121P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-875-8383

; TELEFAX: 215-875-8394

; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-343-443B-74

Query Match 31.1%; Score 30.5; DB 2; Length 11;
Best Local Similarity 46.2%; Pred. No. 98;
Matches 6; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

Qy 4 PDVEKPDLPFFQV 16
||: || |:|:
Db 1 PDL---DLDPYQI 10

RESULT 9

US-08-343-443B-94

; Sequence 94, Application US/08343443B
; Patent No. 5968734

; GENERAL INFORMATION:

; APPLICANT: Aurias, Alain
; APPLICANT: Delattre, Olivier
; APPLICANT: Desmaze, Chantal
; APPLICANT: Melot, Thomas
; APPLICANT: Peter, Martine
; APPLICANT: Floougastel, Beatrice
; APPLICANT: Thomas, Gilles
; APPLICANT: Zucman, Jessica

; TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
; TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
; TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF
CANCEROUS

; TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM
SAID

; TITLE OF INVENTION: TRANSLOCATIONS
; NUMBER OF SEQUENCES: 129

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Weiser & Associates
; STREET: 230 South Fifteenth Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AEDIT 1.0 DOS text editor

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/343,443B
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR93/00494
; FILING DATE: 19-MAY-1993

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/06123
; FILING DATE: 20-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6121P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-343-443B-94

```

```

Query Match          31.1%; Score 30.5; DB 2; Length 11;
Best Local Similarity 46.2%; Pred. No. 98;
Matches      6; Conservative      3; Mismatches      1; Indels      3; Gaps      1;

```

```

Qy      4 PDVEKPDLPFQV 16
        ||:  || |:|:
Db      1 PDL---DLDPYQI 10

```

RESULT 10

```

US-09-914-259-70
; Sequence 70, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human rhinovirus 2
US-09-914-259-70

```

```

Query Match          29.6%; Score 29; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PDLQP 13
        |||||
Db      9 PDLQP 13

```

RESULT 11

US-08-144-121-12

; Sequence 12, Application US/08144121
; Patent No. 5610031
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: Blk CHAIN OF LAMININ AND METHODS OF USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: BOSTON
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/144,121
; FILING DATE: 27-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: (MGH-0780.0) MGP-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal

US-08-144-121-12

Query Match 29.6%; Score 29; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPD 10
|: ||:| |
Db 1 DENPDIECAD 10

RESULT 12

US-08-735-893-12

; Sequence 12, Application US/08735893
; Patent No. 5914317
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: Blk CHAIN OF LAMININ AND METHODS OF USE

; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, suite 510
 ; CITY: BOSTON
 ; STATE: Massachusetts
 ; COUNTRY: United States
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/735,893
 ; FILING DATE: 18-OCT-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/144,121
 ; FILING DATE: 27-OCT-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Myers, Paul L.
 ; REGISTRATION NUMBER: 35,965
 ; REFERENCE/DOCKET NUMBER: (MGH-0780.1) MGP-021DV
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 227-5941
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 US-08-735-893-12

Query Match 29.6%; Score 29; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPD 10
 | : | | : | |
 Db 1 DENPDIECAD 10

RESULT 13
 US-09-461-697-200
 ; Sequence 200, Application US/09461697
 ; Patent No. 6277974
 ; GENERAL INFORMATION:
 ; APPLICANT: COGENT NEUROSCIENCE, Inc.
 ; APPLICANT: Lo, Donald C.
 ; APPLICANT: Barney, Shawn
 ; APPLICANT: Thomas, Mary Beth
 ; APPLICANT: Portbury, Stuart D.
 ; APPLICANT: Puranam, Kasturi

```

; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 200
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-461-697-200

```

```

Query Match          29.6%;  Score 29;  DB 3;  Length 18;
Best Local Similarity 54.5%;  Pred. No. 2.8e+02;
Matches      6;  Conservative    2;  Mismatches    3;  Indels      0;  Gaps      0;

```

```

Qy      6 VEKPDLPFFQV 16
        :||| || |:
Db      1 MEKPKLQRHQL 11

```

RESULT 14

US-08-190-788A-43

```

; Sequence 43, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
;   APPLICANT: Yanofsky, Stephen D.
;   APPLICANT: Barrett, Ronald W.
;   APPLICANT: Baldwin, David N.
;   APPLICANT: Jacobs, Jeff W.
;   TITLE OF INVENTION: Peptides and Compounds That Bind to the
;   TITLE OF INVENTION: IL-1 Receptor
;   NUMBER OF SEQUENCES: 312
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Affymax Technologies N.V.
;     STREET: 4001 Miranda Avenue
;     CITY: Palo Alto
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/190,788A
;     FILING DATE: 02-FEB-1994
;     CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/847,567
;     FILING DATE: 05-MAR-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Stevens, Lauren L.

```

; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-43

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 15

US-08-190-788A-52

; Sequence 52, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691

; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-52

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 16

US-08-190-788A-284

; Sequence 284, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1


```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 284:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 5
; OTHER INFORMATION: /note= "naphthylalanine."
US-08-190-788A-284

```

```

Query Match          28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches      5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      12 QPFQVQS 18
        ||: |||
Db      6 QPYSVQS 12

```

RESULT 17

```

US-08-383-474B-48
; Sequence 48, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530

```

```

; ATTORNEY/AGENT INFORMATION:
;   NAME: Stevens, Lauren L.
;   REGISTRATION NUMBER: 36,691
;   REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-496-2300
;   TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 48:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 12 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-383-474B-48

```

```

Query Match          28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches      5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      12 QPFQVQS 18
        ||: |||
Db      6 QPYSVQS 12

```

RESULT 18

US-08-383-474B-57

```

; Sequence 57, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
;   APPLICANT: Yanofsky, Stephen D.
;   APPLICANT: Barrett, Ronald W.
;   APPLICANT: Baldwin, David N.
;   APPLICANT: Jacobs, Jeff W.
;   TITLE OF INVENTION: Peptides and Compounds That Bind to
;   TITLE OF INVENTION: the IL-1 Receptor
;   NUMBER OF SEQUENCES: 314
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend & Townsend & Crew LLP
;     STREET: Two Embarcadero Center, 8th Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/383,474B
;   FILING DATE: 01-FEB-1995
;   CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/190,788
;   FILING DATE: 02-FEB-1994
;   CLASSIFICATION: 530

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-474B-57

Query Match 28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 19

US-08-383-474B-285
; Sequence 285, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 285:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 5
; OTHER INFORMATION: /note= "naphthylalanine."
US-08-383-474B-285

```

```

Query Match          28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches      5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      12 QPFQVQS 18
        ||: |||
Db      6 QPYSVQS 12

```

RESULT 20

US-08-465-391A-43

```

; Sequence 43, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillipe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331viel, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-43

```

```

Query Match          28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches      5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      12 QPFQVQS 18
        ||: |||
Db      6 QPYSVQS 12

```

RESULT 21

US-08-465-391A-52

```

; Sequence 52, Application US/08465391A
; Patent No. 5786331

```

GENERAL INFORMATION:

```

; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillipe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA

```

```

; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331viel, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-52

```

```

Query Match          28.6%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches      5; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      12 QPFQVQS 18
        ||: |||
Db      6 QPYSVQS 12

```

RESULT 22

US-08-465-391A-284

```

; Sequence 284, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillipe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor

```

```

;   NUMBER OF SEQUENCES:  405
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Townsend and Townsend and Crew
;     STREET:  One Market Plaza, Steuart Tower, Suite 2000
;     CITY:  San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94105
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/465,391A
;     FILING DATE:  05-JUN-1995
;     CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/373,474
;     FILING DATE:  01-FEB-1995
;     CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/190,788
;     FILING DATE:  02-FEB-1994
;     CLASSIFICATION:  514
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  No. 5786331viel, Vern
;     REGISTRATION NUMBER:  32,483
;     REFERENCE/DOCKET NUMBER:  16528A-001840/1019.2A
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415-326-2400
;     TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  284:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  12 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Region
;       LOCATION:  5
;       OTHER INFORMATION:  /note= "naphthylalanine."
US-08-465-391A-284

```

```

Query Match          28.6%;  Score 28;  DB 1;  Length 12;
Best Local Similarity 71.4%;  Pred. No. 2.6e+02;
Matches      5;  Conservative    1;  Mismatches    1;  Indels      0;  Gaps      0;

```

```

Qy      12 QPFQVQS 18
        ||: |||
Db      6 QPYSVQS 12

```

```

RESULT 23
US-08-464-538B-43
; Sequence 43, Application US/08464538B

```

```

; Patent No. 5861476
; GENERAL INFORMATION:
;   APPLICANT:  Barrett, Ronald W.
;   APPLICANT:  Yanofsky, Stephen D.
;   APPLICANT:  Baldwin, David
;   APPLICANT:  Jacobs, Jeff W.
;   APPLICANT:  Bovy, Phillipe R.
;   APPLICANT:  Leahy, Ellen M.
;   APPLICANT:  Pottorf, Richard S.
;   TITLE OF INVENTION:  Peptides and Compounds That Bind to the
;   TITLE OF INVENTION:  IL-1 Receptor
;   NUMBER OF SEQUENCES:  402
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Townsend and Townsend and Crew LLP
;     STREET:    Two Embarcadero Center, 8th Floor
;     CITY:      San Francisco
;     STATE:     California
;     COUNTRY:   USA
;     ZIP:       94111
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:    IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:    PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/464,538B
;     FILING DATE:       05-JUN-1995
;     CLASSIFICATION:    514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/373,474
;     FILING DATE:        01-FEB-1995
;     CLASSIFICATION:     514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/190,788
;     FILING DATE:        02-FEB-1994
;     CLASSIFICATION:     514
;   ATTORNEY/AGENT INFORMATION:
;     NAME:              Smith, William M.
;     REGISTRATION NUMBER: 30,223
;     REFERENCE/DOCKET NUMBER: 16528A-001810
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:         415-326-2400
;     TELEFAX:           415-326-2422
;   INFORMATION FOR SEQ ID NO: 43:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 12 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-08-464-538B-43

```

```

Query Match          28.6%;  Score 28;  DB 2;  Length 12;
Best Local Similarity 71.4%;  Pred. No. 2.6e+02;
Matches      5;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;

```

```

Qy      /      12 QPFQVQS 18

```


Db ||: |||
 6 QPYSVQS 12

RESULT 24

US-08-464-538B-52

; Sequence 52, Application US/08464538B

; Patent No. 5861476

; GENERAL INFORMATION:

; APPLICANT: Barrett, Ronald W.

; APPLICANT: Yanofsky, Stephen D.

; APPLICANT: Baldwin, David

; APPLICANT: Jacobs, Jeff W.

; APPLICANT: Bovy, Phillipe R.

; APPLICANT: Leahy, Ellen M.

; APPLICANT: Pottorf, Richard S.

; TITLE OF INVENTION: Peptides and Compounds That Bind to the

; TITLE OF INVENTION: IL-1 Receptor

; NUMBER OF SEQUENCES: 402

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,538B

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/373,474

; FILING DATE: 01-FEB-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/190,788

; FILING DATE: 02-FEB-1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 16528A-001810

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 52:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-464-538B-52

Query Match 28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 25

US-08-464-538B-283

; Sequence 283, Application US/08464538B
; Patent No. 5861476

; GENERAL INFORMATION:

; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillipe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,538B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528A-001810

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422

```

; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 12 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
;   NAME/KEY: Region
;   LOCATION: 5
; OTHER INFORMATION: /note= "naphthylalanine."
US-08-464-538B-283

```

```

Query Match          28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches      5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      12 QPFQVQS 18
        ||: |||
Db      6 QPYSVQS 12

```

RESULT 26

US-08-463-076E-87

```

; Sequence 87, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
;   APPLICANT: Barrett, Ronald W.
;   APPLICANT: Yanofsky, Stephen D.
;   TITLE OF INVENTION: Peptides and Compounds That Bind to the
;   TITLE OF INVENTION: IL-1 Receptor
;   NUMBER OF SEQUENCES: 392
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Center, Eighth Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/463,076E
;     FILING DATE: 05-JUN-1995
;     CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Snyder, Joseph R.
;     REGISTRATION NUMBER: 39,381
;     REFERENCE/DOCKET NUMBER: 16528A-001850US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 576-0200
;     TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-076E-87

Query Match 28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 27

US-08-463-076E-96

; Sequence 96, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-076E-96

Query Match 28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 28

US-08-463-076E-357

; Sequence 357, Application US/08463076E

; Patent No. 5880096

; GENERAL INFORMATION:

; APPLICANT: Barrett, Ronald W.

; APPLICANT: Yanofsky, Stephen D.

; TITLE OF INVENTION: Peptides and Compounds That Bind to the

; TITLE OF INVENTION: IL-1 Receptor

; NUMBER OF SEQUENCES: 392

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/463,076E

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Snyder, Joseph R.

; REGISTRATION NUMBER: 39,381

; REFERENCE/DOCKET NUMBER: 16528A-001850US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 357:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 5

; OTHER INFORMATION: /product= "OTHER"

; OTHER INFORMATION: /note= "Xaa = naphthylalanine"

US-08-463-076E-357

Query Match 28.6%; Score 28; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 29

US-09-428-082B-673
; Sequence 673, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-09-428-082B-673

Query Match 28.6%; Score 28; DB 4; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 30

US-09-428-082B-683
; Sequence 683, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371

; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 683
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-09-428-082B-683

Query Match 28.6%; Score 28; DB 4; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 31

US-09-428-082B-958
; Sequence 958, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 958
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: Position 5, Xaa = naphthylalanine
US-09-428-082B-958

Query Match 28.6%; Score 28; DB 4; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 32
 US-08-347-335A-13
 ; Sequence 13, Application US/08347335A
 ; Patent No. 5856163
 ; GENERAL INFORMATION:
 ; APPLICANT: Hashida, Miyoko
 ; APPLICANT: Abo, Masanobu
 ; APPLICANT: Takamura, Yukiko
 ; APPLICANT: Kirk, Ole
 ; APPLICANT: Halkier, Torben
 ; APPLICANT: Pedersen, Sven
 ; APPLICANT: Patkar, Shamkant A.
 ; APPLICANT: Hansen, Mogens T.
 ; TITLE OF INVENTION: NOVEL ENZYMES
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5856163o No. 5856163disk of No. 5856163th America, Inc.
 ; STREET: 405 Lexington Avenue, 64th Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/347,335A
 ; FILING DATE: 22-DEC-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lambiris, Elias J.
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 3706.204-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-347-335A-13

Query Match 28.6%; Score 28; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 2.8e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KPDLQPF 14
 :||| |:

Db 3 EPDLMPY 9

RESULT 33

US-08-467-083-53
; Sequence 53, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-467-083-53

Query Match 28.6%; Score 28; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDQL 12
|| | :||::
Db 5 QPEYVNQPDVR 15

RESULT 34

US-08-414-417B-53

; Sequence 53, Application US/08414417B

```

; Patent No. 5801005
; GENERAL INFORMATION:
;   APPLICANT: Cheever, Martin A.
;   APPLICANT: Disis, Mary L.
;   TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;   TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
THE
;   TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
;   NUMBER OF SEQUENCES: 69
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Seed and Berry LLP
;     STREET: 6300 Columbia Center, 701 Fifth Avenue
;     CITY: Seattle
;     STATE: Washington
;     COUNTRY: US
;     ZIP: 98104-7092
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/414,417B
;     FILING DATE: 31-MAR-1995
;     CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Sharkey, Richard G.
;     REGISTRATION NUMBER: 32,629
;     REFERENCE/DOCKET NUMBER: 920010.448C2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (206) 622-4900
;     TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 53:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 15 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
US-08-414-417B-53

```

```

Query Match          28.6%; Score 28; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 3.3e+02;
Matches      5; Conservative      3; Mismatches      3; Indels      0; Gaps      0;

```

```

Qy      2 QPPDVEKPDQLQ 12
      || | :||::
Db      5 QPEYVNQPDVR 15

```

```

RESULT 35
US-08-486-348A-53
; Sequence 53, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
;   APPLICANT: Cheever, Martin A.
;   APPLICANT: Disis, Mary L.
;   TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

```

; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
 THE
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/486,348A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sharkey, Richard G.
 ; REGISTRATION NUMBER: 32,629
 ; REFERENCE/DOCKET NUMBER: 920010.448C6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 53:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-486-348A-53

Query Match 28.6%; Score 28; DB 2; Length 15;
 Best Local Similarity 45.5%; Pred. No. 3.3e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDQL 12
 || | :||:
 Db 5 QPEYVNQPDVR 15

RESULT 36

US-08-468-545B-53

; Sequence 53, Application US/08468545B
 ; Patent No. 5876712

GENERAL INFORMATION:

; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Disis, Mary L.
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
 THE
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP

```

; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-468-545B-53

```

```

Query Match          28.6%; Score 28; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 3.3e+02;
Matches      5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      2 QPPDVEKPDQL 12
        || | :||::
Db      5 QPEYVNQPDVR 15

```

RESULT 37

US-08-466-680B-53

; Sequence 53, Application US/08466680B

; Patent No. 6075122

; GENERAL INFORMATION:

; APPLICANT: Cheever, Martin A.

; APPLICANT: Disis, Mary L.

; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
THE

; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-466-680B-53

```

```

Query Match          28.6%; Score 28; DB 3; Length 15;
Best Local Similarity 45.5%; Pred. No. 3.3e+02;
Matches      5; Conservative      3; Mismatches      3; Indels      0; Gaps      0;

```

```

Qy      2 QPPDVEKPDQ 12
        || | :||::
Db      5 QPEYVNQPDVR 15

```

RESULT 38

US-09-354-533-53

```

; Sequence 53, Application US/09354533
; Patent No. 6664370

```

GENERAL INFORMATION:

```

; APPLICANT: Cheever, Martin A.
;           Disis, Mary L.

```

```

; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;                   FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN

```

WHICH THE

```

;                   HER-2/neu ONCOGENE IS ASSOCIATED

```

```

; NUMBER OF SEQUENCES: 69

```

```

; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092

```

```

; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,533

```

```

;      FILING DATE: 15-Jul-1999
;      CLASSIFICATION: <Unknown>
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Sharkey, Richard G.
;      REGISTRATION NUMBER: 32,629
;      REFERENCE/DOCKET NUMBER: 920010.448C9
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206) 622-4900
;      TELEFAX: (206) 682-6031
;      INFORMATION FOR SEQ ID NO: 53:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 15 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-354-533-53

```

```

Query Match      28.6%;  Score 28;  DB 4;  Length 15;
Best Local Similarity  45.5%;  Pred. No. 3.3e+02;
Matches      5;  Conservative      3;  Mismatches      3;  Indels      0;  Gaps      0;

```

```

Qy      2 QPPDVEKPDQLQ 12
      || | :||::
Db      5 QPEYVNQPDVR 15

```

```

RESULT 39
US-08-190-788A-170
; Sequence 170, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-170

Query Match 28.6%; Score 28; DB 1; Length 16;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 7 QPYSVQS 13

RESULT 40

US-08-383-474B-173
; Sequence 173, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-474B-173

Query Match 28.6%; Score 28; DB 1; Length 16;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 7 QPYSVQS 13

RESULT 41

US-08-465-391A-170

; Sequence 170, Application US/08465391A

; Patent No. 5786331

; GENERAL INFORMATION:

; APPLICANT: Barrett, Ronald W.

; APPLICANT: Yanofsky, Stephen D.

; APPLICANT: Baldwin, David

; APPLICANT: Jacobs, Jeff W.

; APPLICANT: Bovy, Phillipe R.

; APPLICANT: Leahy, Ellen M.

; APPLICANT: Pottorf, Richard S.

; TITLE OF INVENTION: Peptides and Compounds That Bind to the

; TITLE OF INVENTION: IL-1 Receptor

; NUMBER OF SEQUENCES: 405

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/465,391A

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 578633lvie1, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-170

Query Match 28.6%; Score 28; DB 1; Length 16;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 7 QPYSVQS 13

RESULT 42

US-08-464-538B-170

; Sequence 170, Application US/08464538B

; Patent No. 5861476

; GENERAL INFORMATION:

; APPLICANT: Barrett, Ronald W.

; APPLICANT: Yanofsky, Stephen D.

; APPLICANT: Baldwin, David

; APPLICANT: Jacobs, Jeff W.

; APPLICANT: Bovy, Phillipe R.

; APPLICANT: Leahy, Ellen M.

; APPLICANT: Pottorf, Richard S.

; TITLE OF INVENTION: Peptides and Compounds That Bind to the

; TITLE OF INVENTION: IL-1 Receptor

; NUMBER OF SEQUENCES: 402

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/464,538B
;   FILING DATE:  05-JUN-1995
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/373,474
;   FILING DATE:  01-FEB-1995
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/190,788
;   FILING DATE:  02-FEB-1994
;   CLASSIFICATION:  514
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Smith, William M.
;   REGISTRATION NUMBER:  30,223
;   REFERENCE/DOCKET NUMBER:  16528A-001810
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-326-2400
;   TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  170:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  16 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-464-538B-170

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Query Match          28.6%;  Score 28;  DB 2;  Length 16;
Best Local Similarity 71.4%;  Pred. No. 3.5e+02;
Matches      5;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

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Qy      12 QPFQVQS 18
        ||: |||
Db      7 QPYSVQS 13

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RESULT 43

US-08-463-076E-223

; Sequence 223, Application US/08463076E

; Patent No. 5880096

; GENERAL INFORMATION:

; APPLICANT: Barrett, Ronald W.

; APPLICANT: Yanofsky, Stephen D.

; TITLE OF INVENTION: Peptides and Compounds That Bind to the

; TITLE OF INVENTION: IL-1 Receptor

; NUMBER OF SEQUENCES: 392

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 223:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-076E-223

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Query Match          28.6%; Score 28; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches      5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      12 QPFQVQS 18
        ||: |||
Db      7 QPYSVQS 13

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RESULT 44
US-09-428-082B-786
; Sequence 786, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 786
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-09-428-082B-786

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Query Match 28.6%; Score 28; DB 4; Length 16;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 7 QPYSVQS 13

RESULT 45

US-08-190-788A-169

; Sequence 169, Application US/08190788A

; Patent No. 5608035

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Stephen D.

; APPLICANT: Barrett, Ronald W.

; APPLICANT: Baldwin, David N.

; APPLICANT: Jacobs, Jeff W.

; TITLE OF INVENTION: Peptides and Compounds That Bind to the

; TITLE OF INVENTION: IL-1 Receptor

; NUMBER OF SEQUENCES: 312

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Affymax Technologies N.V.

; STREET: 4001 Miranda Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/190,788A

; FILING DATE: 02-FEB-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/847,567

; FILING DATE: 05-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Stevens, Lauren L.

; REGISTRATION NUMBER: 36,691

; REFERENCE/DOCKET NUMBER: 1019.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-496-2300

; TELEFAX: 415-424-0832

; INFORMATION FOR SEQ ID NO: 169:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-190-788A-169

Query Match 28.6%; Score 28; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 8 QPYSVQS 14

RESULT 46

US-08-190-788A-230

; Sequence 230, Application US/08190788A

; Patent No. 5608035

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Stephen D.

; APPLICANT: Barrett, Ronald W.

; APPLICANT: Baldwin, David N.

; APPLICANT: Jacobs, Jeff W.

; TITLE OF INVENTION: Peptides and Compounds That Bind to the

; TITLE OF INVENTION: IL-1 Receptor

; NUMBER OF SEQUENCES: 312

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Affymax Technologies N.V.

; STREET: 4001 Miranda Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/190,788A

; FILING DATE: 02-FEB-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/847,567

; FILING DATE: 05-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Stevens, Lauren L.

; REGISTRATION NUMBER: 36,691

; REFERENCE/DOCKET NUMBER: 1019.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-496-2300

; TELEFAX: 415-424-0832

; INFORMATION FOR SEQ ID NO: 230:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-190-788A-230

Query Match 28.6%; Score 28; DB 1; Length 17;

Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 8 QPYSVQS 14

RESULT 47

US-08-190-788A-233

; Sequence 233, Application US/08190788A

; Patent No. 5608035

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Stephen D.

; APPLICANT: Barrett, Ronald W.

; APPLICANT: Baldwin, David N.

; APPLICANT: Jacobs, Jeff W.

; TITLE OF INVENTION: Peptides and Compounds That Bind to the

; TITLE OF INVENTION: IL-1 Receptor

; NUMBER OF SEQUENCES: 312

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Affymax Technologies N.V.

; STREET: 4001 Miranda Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/190,788A

; FILING DATE: 02-FEB-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/847,567

; FILING DATE: 05-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Stevens, Lauren L.

; REGISTRATION NUMBER: 36,691

; REFERENCE/DOCKET NUMBER: 1019.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-496-2300

; TELEFAX: 415-424-0832

; INFORMATION FOR SEQ ID NO: 233:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-190-788A-233

Query Match 28.6%; Score 28; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 8 QPYSVQS 14

RESULT 48

US-08-190-788A-234

; Sequence 234, Application US/08190788A

; Patent No. 5608035

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Stephen D.

; APPLICANT: Barrett, Ronald W.

; APPLICANT: Baldwin, David N.

; APPLICANT: Jacobs, Jeff W.

; TITLE OF INVENTION: Peptides and Compounds That Bind to the

; TITLE OF INVENTION: IL-1 Receptor

; NUMBER OF SEQUENCES: 312

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Affymax Technologies N.V.

; STREET: 4001 Miranda Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/190,788A

; FILING DATE: 02-FEB-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/847,567

; FILING DATE: 05-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Stevens, Lauren L.

; REGISTRATION NUMBER: 36,691

; REFERENCE/DOCKET NUMBER: 1019.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-496-2300

; TELEFAX: 415-424-0832

; INFORMATION FOR SEQ ID NO: 234:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-190-788A-234

Query Match 28.6%; Score 28; DB 1; Length 17;

Best Local Similarity 71.4%; Pred. No. 3.8e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 8 QPYSVQS 14

RESULT 49

US-08-383-474B-172

; Sequence 172, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 172:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-474B-172

Query Match 28.6%; Score 28; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 8 QPYSVQS 14

RESULT 50

US-08-383-474B-233

; Sequence 233, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 233:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-474B-233

Query Match 28.6%; Score 28; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 8 QPYSVQS 14

Search completed: July 4, 2004, 04:48:46
Job time : 12.2836 secs

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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:35:16 ; Search time 13.8358 Seconds
(without alignments)
125.142 Million cell updates/sec

Title: US-09-641-802-3
Perfect score: 98
Sequence: 1 DQPPDVEKPDLPFFQVQS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2898

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	30	30.6	10	2	C35389	urease (EC 3.5.1.5
2	29	29.6	15	2	S20410	protein kinase (EC
3	29	29.6	15	2	PA0041	plastoquinol-plast
4	28.5	29.1	17	2	A42920	fatty acid ethyl e
5	27	27.6	9	2	S66419	tetrameric protein
6	25.5	26.0	17	4	I51887	hypothetical EWSR1
7	25	25.5	15	2	A60221	apolipoprotein A-I
8	24	24.5	10	2	B61218	alpha-gliadin 6Ha
9	24	24.5	14	2	A61362	bradykinin-like pe
10	24	24.5	18	2	PN0149	beta-Gliadine 13 -
11	24	24.5	18	2	A54195	Na+/K+-exchanging
12	23	23.5	9	2	S77984	cytochrome-c oxida
13	23	23.5	11	2	A61365	phyllokinin - Rohd

14	23	23.5	12	2	A61360	vespakinin M - hor
15	23	23.5	12	2	A61359	vespakinin X - hor
16	23	23.5	13	2	G61458	Ig lambda chain V-
17	23	23.5	15	2	PA0088	protein QF200051 -
18	23	23.5	18	2	A60915	enkephalin-degradi
19	22	22.4	12	2	S07436	tachykinin - Afric
20	22	22.4	16	2	JH0517	insulin-like growt
21	21	21.4	11	2	S78765	ribosomal protein
22	21	21.4	12	2	S10059	tachykinin - Afric
23	21	21.4	15	2	PN0665	dystrophin-associa
24	21	21.4	16	2	A60551	leukocyte elastase
25	21	21.4	17	2	B44873	caldesmon - rabbit
26	21	21.4	18	2	S26664	microtubule-associ
27	20	20.4	8	2	I57532	gene TnIslow prote
28	20	20.4	9	2	A61363	bradykinin - commo
29	20	20.4	9	2	D48186	ATPase Rl subunit
30	20	20.4	9	2	S65433	bradykinin - horn
31	20	20.4	9	2	A43065	hydroxyproline-3-b
32	20	20.4	10	2	A60476	S-layer protein -
33	20	20.4	11	2	YHRT	morphogenetic neur
34	20	20.4	11	2	YHHU	morphogenetic neur
35	20	20.4	11	2	YHBO	morphogenetic neur
36	20	20.4	11	2	YHXAE	morphogenetic neur
37	20	20.4	11	2	YHJFHY	morphogenetic neur
38	20	20.4	11	2	S13279	Ile-Ser-bradykinin
39	20	20.4	12	2	C64030	hypothetical prote
40	20	20.4	13	2	S15755	actin 7 - soybean
41	20	20.4	13	2	A61361	bradykinin-like pe
42	20	20.4	15	2	A49155	vasotocin-associat
43	20	20.4	15	2	I49407	placental calcium-
44	20	20.4	15	2	B39109	hypothetical 1.5K
45	20	20.4	15	2	F57789	gallbladder stone
46	20	20.4	17	1	A61339	vespulinin 1 - e
47	20	20.4	17	2	B61334	trypsin (EC 3.4.21
48	20	20.4	17	2	S15754	actin 6 - soybean
49	20	20.4	17	2	S05033	photosystem II pro
50	20	20.4	17	2	S59481	hydroxyproline-ric
51	20	20.4	18	2	S29166	quinaldine oxidore
52	20	20.4	18	2	A56798	dermatan sulfate p
53	19.5	19.9	11	2	C37196	bradykinin-potenti
54	19.5	19.9	11	2	D37196	bradykinin-potenti
55	19.5	19.9	15	4	I38032	hypothetical MN1/T
56	19	19.4	7	2	S71299	ICL2 protein - Par
57	19	19.4	7	2	PT0283	Ig heavy chain CRD
58	19	19.4	8	2	I48935	apolipoprotein A-I
59	19	19.4	9	2	A61358	bradykinin-like pe
60	19	19.4	9	2	A61057	Thr-6 bradykinin -
61	19	19.4	9	2	A26744	bradykinin-like pe
62	19	19.4	9	2	A60579	bradykinin-like pe
63	19	19.4	9	2	G58502	kidney and bladder
64	19	19.4	10	2	A32543	cardioexcitatory n
65	19	19.4	11	2	B26744	megascoliakinin -
66	19	19.4	11	2	D45900	complement C3b rec
67	19	19.4	12	2	S07206	kassinin - Senegal
68	19	19.4	12	2	T46794	hypothetical prote
69	19	19.4	12	2	S27024	Na+/K+-exchanging
70	19	19.4	12	2	S27023	Na+/K+-exchanging

71	19	19.4	13	2	S21152	tryptophyllin-rela
72	19	19.4	13	2	T08533	hypothetical prote
73	19	19.4	13	2	S22995	hypothetical prote
74	19	19.4	13	2	A33660	osteoclast functio
75	19	19.4	15	2	PS0185	27K protein A 3.4/
76	19	19.4	15	2	PC1313	small granule S6 c
77	19	19.4	15	2	PS0221	gastrin-releasing
78	19	19.4	16	2	D49655	T-cell-receptor be
79	19	19.4	16	2	PH0759	T-cell receptor be
80	19	19.4	17	2	S50901	chlorophyll a/b-bi
81	19	19.4	17	2	S10786	enamelin, 26K - bo
82	19	19.4	17	2	S78421	ribosomal protein
83	18.5	18.9	11	1	XASNBA	bradykinin-potenti
84	18.5	18.9	15	2	S29207	avenin gamma-4 - o
85	18.5	18.9	15	2	PW0004	chlorophyll a/b-bi
86	18	18.4	7	2	I48086	DNA topoisomerase
87	18	18.4	8	2	PT0030	inulinase (EC 3.2.
88	18	18.4	9	2	A61620	locustamyotropin I
89	18	18.4	9	2	B46250	alpha-adaptin - bo
90	18	18.4	10	2	A61007	hementin (EC 3.4.-
91	18	18.4	11	2	PQ0231	beta-glucosidase (
92	18	18.4	11	2	S21127	precorrin methyltr
93	18	18.4	11	2	PS0257	31K protein 3208 -
94	18	18.4	11	2	D56979	collagen alpha 1(I
95	18	18.4	12	2	S36899	ribosomal protein
96	18	18.4	12	2	E44787	calliMIRFamide 1 -
97	18	18.4	12	2	S51737	T-cell receptor be
98	18	18.4	12	2	S71380	lebetin 1 isoform
99	18	18.4	13	2	A05174	tryptophyllin-13 -
100	18	18.4	13	2	I84603	deoxynucleotidyltr

ALIGNMENTS

RESULT 1

C35389

urease (EC 3.5.1.5) 6K chain - *Morganella morganii* (fragment)

C;Species: *Morganella morganii*

C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 23-Jun-1993

C;Accession: C35389

R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.

J. Bacteriol. 172, 3073-3080, 1990

A;Title: *Morganella morganii* urease: purification, characterization, and isolation of gene sequences.

A;Reference number: A35389; MUID:90264298; PMID:2345135

A;Accession: C35389

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <HUA>

C;Keywords: hydrolase

Query Match 30.6%; Score 30; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 82;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPDVEK 8

Db 5 PPEVEK 10

RESULT 2

S20410

protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)

N;Alternate names: LHCII protein kinase

C;Species: chloroplast *Spinacia oleracea* (spinach)

C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C;Accession: S20410

R;Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.

FEBS Lett. 298, 33-35, 1992

A;Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cytochrome complex.

A;Reference number: S20410; MUID:92183823; PMID:1544419

A;Accession: S20410

A;Molecule type: protein

A;Residues: 1-15 <GAL>

C;Genetics:

A;Genome: chloroplast

C;Function:

A;Description: is responsible for the regulation of energy distribution between photosystem I and II

A;Note: does not exhibit redox-controlled activation

C;Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphotransferase; photosynthesis; thylakoid

Query Match 29.6%; Score 29; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PDVEKPD 11
 | | | | |
Db 5 PDVEKSTL 12

RESULT 3

PA0041

plastoquinol-plastocyanin reductase (EC 1.10.99.1) - *Arabidopsis thaliana* (fragment)

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 03-Jun-2002

C;Accession: PA0041

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A;Description: Separation and characterization of *Arabidopsis* proteins by two-dimensional gel electrophoresis.

A;Reference number: PA0001

A;Accession: PA0041

A;Molecule type: protein

A;Residues: 1-15 <KAM>

A;Experimental source: leaf

C;Keywords: oxidoreductase

Query Match 29.6%; Score 29; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQPPDVEK 8
|: ||: ||
Db 7 DRVPDMEK 14

RESULT 4

A42920

fatty acid ethyl ester synthase-II - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995

C;Accession: A42920

R;Bora, P.S.; Wu, X.; Spilburg, C.A.; Lange, L.G.

J. Biol. Chem. 267, 13217-13221, 1992

A;Title: Purification and characterization of fatty acid ethyl ester synthase-II from human myocardium.

A;Reference number: A42920; MUID:92317032; PMID:1618826

A;Accession: A42920

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-17 <BOR>

A;Experimental source: myocardium

A;Note: sequence extracted from NCBI backbone (NCBIP:107742)

Query Match 29.1%; Score 28.5; DB 2; Length 17;
Best Local Similarity 46.2%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

Qy 1 DQPPDVEKPDLQP 13
: ||| || |
Db 1 EDPPD---PDTTP 10

RESULT 5

S66419

tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)

C;Species: Spinacia oleracea (spinach)

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997

C;Accession: S66419

R;Kuwabara, T.

FEBS Lett. 371, 195-198, 1995

A;Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spinach thylakoids: structural similarities between the protease and polyphenol oxidase.

A;Reference number: S66419; MUID:95402209; PMID:7672127

A;Accession: S66419

A;Molecule type: protein

A;Residues: 1-9 <KUW>

Query Match 27.6%; Score 27; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PDVEK 8
||||

RESULT 6

I51887

hypothetical EWSR1/FLI1 mutant fusion protein, type 1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000

C;Accession: I51887

R;Downing, J.R.; Head, D.R.; Parham, D.M.; Douglass, E.C.; Hulshof, M.G.; Link, M.P.; Motroni, T.A.; Grier, H.E.; Curcio-Brint, A.M.; Shapiro, D.N.

Am. J. Pathol. 143, 1294-1300, 1993

A;Title: Detection of the (11;22)(q24;q12) translocation of Ewing's sarcoma and peripheral neuroectodermal tumor by reverse transcription polymerase chain reaction.

A;Reference number: I51887; MUID:94056652; PMID:8238248

A;Accession: I51887

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-17 <DOW>

A;Cross-references: GB:S66911; NID:g440935; PIDN:AAB28655.1; PID:g440936

C;Comment: This sequence is the chimeric product of a translocation mutation.

C;Genetics:

A;Gene: EWSR1/FLI1; EWS/FLI-1

A;Map position: 22q12/11q24

C;Keywords: fusion protein

Query Match 26.0%; Score 25.5; DB 4; Length 17;
Best Local Similarity 46.2%; Pred. No. 7.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 1 DQPPDVEKPDLP 13

|: ||: || |

Db 7 DEGPDL---DLDP 16

RESULT 7

A60221

apolipoprotein A-I - common carp (fragment)

C;Species: Cyprinus carpio (common carp)

C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Dec-1993

C;Accession: A60221

R;Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.

J. Neurochem. 55, 1237-1243, 1990

A;Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve regeneration.

A;Reference number: A60221; MUID:90376100; PMID:2118944

A;Accession: A60221

A;Molecule type: protein

A;Residues: 1-15 <HAR>

A;Note: protein from plasma and from optic nerve yielded the same sequence

C;Keywords: lipid binding; lipoprotein

Query Match 25.5%; Score 25; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQPP 4
| | | |
Db 1 DQPP 4

RESULT 8

B61218

alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)

C;Species: Haynaldia villosa, Dasypyrum villosum

C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999

C;Accession: B61218

R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.

Biochem. Genet. 29, 207-211, 1991

A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa Schur (syn. Dasypyrum villosum L.).

A;Reference number: A61218; MUID:91315394; PMID:1859356

A;Accession: B61218

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <SHE>

C;Keywords: seed; storage protein

Query Match 24.5%; Score 24; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 7.1e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13
| | | |
Db 3 VPVPQLPQ 10

RESULT 9

A61362

bradykinin-like peptide III - Japanese pond frog

C;Species: Rana nigromaculata (Japanese pond frog)

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000

C;Accession: A61362

R;Nakajima, T.

Chem. Pharm. Bull. 16, 2088-2089, 1968

A;Title: On the third active peptide on smooth muscle in the skin of Rana nigromaculata hallowell.

A;Reference number: A61362; MUID:69117202; PMID:5751736

A;Accession: A61362

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <NAK>

C;Superfamily: unassigned animal peptides

C;Keywords: skin

Query Match 24.5%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16
| | | |
Db 3 PGFSPFRV 10

RESULT 10

PN0149

beta-Gliadine 13 - Aegilops longissima (fragment)

C;Species: Aegilops longissima

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PN0149

R;Odintsova, T.I.; Egorov, T.A.

Biokhimiia 55, 509-516, 1990

A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of polyploid wheat genomes.

A;Reference number: PN0146; MUID:90283493; PMID:2354218

A;Accession: PN0149

A;Molecule type: protein

A;Residues: 1-18 <ODI>

A;Experimental source: strain K-202

C;Superfamily: gliadin

Query Match 24.5%; Score 24; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13
| | |||
Db 3 VPVPQLQP 10

RESULT 11

A54195

Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)

C;Species: Squalus acanthias (spiny dogfish)

C;Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Apr-2002

C;Accession: A54195

R;Esmann, M.; Karlsh, S.J.; Sottrup-Jensen, L.; Marsh, D.

Biochemistry 33, 8044-8050, 1994

A;Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase from shark rectal glands.

A;Reference number: A54195; MUID:94297020; PMID:8025109

A;Accession: A54195

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <ESM>

A;Experimental source: rectal gland

A;Note: sequence extracted from NCBI backbone (NCBIP:149363)

C;Keywords: hydrolase

Query Match 24.5%; Score 24; DB 2; Length 18;
Best Local Similarity 23.5%; Pred. No. 1.4e+03;
Matches 4; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLPFQVQ 17
| | : | | : :
Db 1 DGPNALTPPPTTPYDIK 17

RESULT 12

S77984

cytochrome-c oxidase (EC 1.9.3.1) chain VIa - bigeye tuna (fragment)
 C;Species: Thunnus obesus (bigeye tuna)
 C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
 C;Accession: S77984
 R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
 submitted to the Protein Sequence Database, June 1997
 A;Reference number: S77980
 A;Accession: S77984
 A;Molecule type: protein
 A;Residues: 1-9 <ARN>
 A;Experimental source: heart
 C;Genetics:
 A;Genome: nuclear
 C;Function:
 A;Pathway: oxidative phosphorylation; respiratory chain
 C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; transmembrane protein

Query Match 23.5%; Score 23; DB 2; Length 9;
 Best Local Similarity 37.5%; Pred. No. 2.8e+05;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 7 EKPDLQPF 14
 |:|: |:
 Db 2 EQPEFVPY 9

RESULT 13

A61365
 phyllokinin - Rohde's leaf frog
 N;Alternate names: bradykinyl-isoleucyl-tyrosine O-sulfate
 C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
 C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
 C;Accession: A61365
 R;Anastasi, A.; Bertaccini, G.; Erspamer, V.
 Br. J. Pharmacol. 27, 479-485, 1966
 A;Title: Pharmacological data on phyllokinin (bradykinyl-isoleucyl-tyrosine O-sulphate) and bradykinyl-isoleucyl-tyrosine.
 A;Reference number: A61365; MUID:67179312; PMID:5970899
 A;Accession: A61365
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-11 <ANA>
 C;Superfamily: unassigned animal peptides
 C;Keywords: sulfoprotein
 F;11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 23.5%; Score 23; DB 2; Length 11;
 Best Local Similarity 37.5%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16
 | ||:
 Db 3 PGFSPFRI 10

RESULT 14

A61360

vespakinin M - hornet (*Vespa mandarinia*)

C;Species: *Vespa mandarinia*

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000

C;Accession: A61360

R;Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.

Chem. Pharm. Bull. 24, 2896-2897, 1976

A;Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the venom of *Vespa mandarinia* Smith.

A;Reference number: A61360; MUID:77114342; PMID:1017116

A;Accession: A61360

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <KIS>

C;Superfamily: unassigned animal peptides

C;Keywords: hydroxyproline; venom

F;4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 23.5%; Score 23; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16

| ||::

Db 4 PGFSPFRI 11

RESULT 15

A61359

vespakinin X - hornet (*Vespa xanthoptera*)

C;Species: *Vespa xanthoptera*

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000

C;Accession: A61359

R;Yasuhara, T.; Yoshida, H.; Nakajima, T.

Chem. Pharm. Bull. 25, 936-941, 1977

A;Title: Chemical investigation of the hornet (*Vespa xanthoptera* Cameron) venom. The structure of a new bradykinin analogue vespakinin-X.

A;Reference number: A61359; MUID:87187853; PMID:264186

A;Accession: A61359

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <YAS>

C;Superfamily: unassigned animal peptides

C;Keywords: venom

Query Match 23.5%; Score 23; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16

| ||::

Db 4 PGFSPFRI 11

RESULT 16

G61458

Ig lambda chain V-II region (AZI) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996

C;Accession: G61458; PL0159

R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.

J. Exp. Med. 170, 1551-1558, 1989

A;Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associated glycoprotein and characterization of the variability subgroup of their heavy and light chains.

A;Reference number: A61458; MUID:90039128; PMID:2478651

A;Accession: G61458

A;Molecule type: protein

A;Residues: 1-13 <BRO>

C;Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycoprotein.

C;Keywords: heterotetramer; immunoglobulin

```
Query Match          23.5%;  Score 23;  DB 2;  Length 13;
Best Local Similarity 80.0%;  Pred. No. 1.4e+03;
Matches      4;  Conservative    0;  Mismatches    1;  Indels      0;  Gaps      0;
```

```
Qy      2 QPPDV 6
        ||| |
Db      6 QPPSV 10
```

RESULT 17

PA0088

protein QF200051 - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C;Accession: PA0088

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A. submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichisides proteins.

A;Reference number: PA0051

A;Accession: PA0088

A;Molecule type: protein

A;Residues: 1-15 <CHO>

```
Query Match          23.5%;  Score 23;  DB 2;  Length 15;
Best Local Similarity 44.4%;  Pred. No. 1.6e+03;
Matches      4;  Conservative    1;  Mismatches    4;  Indels      0;  Gaps      0;
```

```
Qy      2 QPPDVEKPD 10
        | ||:  |
Db      1 QKPDIPXDD 9
```

RESULT 18

A60915

enkephalin-degrading aminopeptidase (EC 3.4.-.-), puromycin-sensitive - rat (fragment)

N;Alternate names: aminoenkephalinase; aminopeptidase MII

C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
C;Accession: A60915
R;Dyer, S.H.; Slaughter, C.A.; Orth, K.; Moomaw, C.R.; Hersh, L.B.
J. Neurochem. 54, 547-554, 1990
A;Title: Comparison of the soluble and membrane-bound forms of the puromycin-sensitive enkephalin-degrading aminopeptidases from rat.
A;Reference number: A60915; MUID:90132681; PMID:2299352
A;Accession: A60915
A;Molecule type: protein
A;Residues: 1-18 <DYE>
A;Note: this sequence represents the N-terminus of both soluble and membrane-associated forms
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: hydrolase

Query Match 23.5%; Score 23; DB 2; Length 18;
Best Local Similarity 42.9%; Pred. No. 2e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
|: :||:
Db 1 PEKRPFE 7

RESULT 19

S07436

tachykinin - African tree frog (Kassina maculata)

N;Alternate names: hylambatin

C;Species: Kassina maculata

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Sep-2000

C;Accession: S07436

R;Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.

Biomed. Res. 2, 613-617, 1981

A;Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, in the skin of the African rhacophorid frog Hylambates maculatus.

A;Reference number: S07436

A;Accession: S07436

A;Molecule type: protein

A;Residues: 1-12 <YAS>

A;Experimental source: skin

A;Note: the source is designated as Hylambates maculatus

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 22.4%; Score 22; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPDVEK 8
||| ::
Db 2 PPDPDR 7

RESULT 20

JH0517

insulin-like growth factor-binding protein 4 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Nov-2003
C;Accession: JH0517
R;Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991
A;Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth factor-binding proteins in porcine serum.
A;Reference number: JH0515; MUID:92109718; PMID:1722398
A;Accession: JH0517
A;Molecule type: protein
A;Residues: 1-16 <COL>
A;Experimental source: serum
C;Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat homology

Query Match 22.4%; Score 22; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPDVEK 8
|| ||
Db 8 PPSEK 13

RESULT 21

S78765

ribosomal protein MRP-S24, mitochondrial - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78765
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Accession: S78765
A;Molecule type: protein
A;Residues: 1-11 <GRA>
C;Keywords: mitochondrion
F;1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 21.4%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DQPPDVEK 8
| | | : |
Db 4 DVPKDLTK 11

RESULT 22

S10059

tachykinin - African tree frog (Kassina maculata)
N;Alternate names: hylambates-kassinin
C;Species: Kassina maculata
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Sep-2000
C;Accession: S10059
R;Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.

Biomed. Res. 2, 613-617, 1981

A;Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, in the skin of the African rhacophorid frog Hylambates maculatus.

A;Reference number: S07436

A;Accession: S10059

A;Molecule type: protein

A;Residues: 1-12 <YAS>

A;Experimental source: skin

A;Note: the source is designated as Hylambates maculatus

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 21.4%; Score 21; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 DVEKPD 10
| |||
Db 1 DEPKPD 6

RESULT 23

PN0665

dystrophin-associated glycoprotein A3a-IV - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C;Accession: PN0665

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in Duchenne muscular dystrophy muscle.

A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0665

A;Molecule type: protein

A;Residues: 1-15 <YOS>

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 21.4%; Score 21; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 3.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
|: |:|
Db 9 PNAPPYQ 15

RESULT 24

A60551

leukocyte elastase (EC 3.4.21.37) - dog (fragment)

C;Species: Canis lupus familiaris (dog)

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 17-Mar-1999

C;Accession: A60551

R;Axelsson, L.; Bergenfeldt, M.; Bjoerk, P.; Olsson, R.; Ohlsson, K.

Scand. J. Clin. Lab. Invest. 50, 35-42, 1990

A;Title: Release of immunoreactive canine leukocyte elastase normally and in endotoxin and pancreatitis shock.

A;Reference number: A60551; MUID:90193608; PMID:1690443

A;Accession: A60551

A;Molecule type: protein

A;Residues: 1-16 <AXE>

C;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; leukocyte; lysosome; serine proteinase

Query Match 21.4%; Score 21; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 3.6e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 8 KPDLPQPFQV 16

:| |||

Db 8 QPHAWPFMV 16

RESULT 25

B44873

caldesmon - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 04-Mar-2000

C;Accession: B44873

R;Ikebe, M.; Hornick, T.

Arch. Biochem. Biophys. 288, 538-542, 1991

A;Title: Determination of the phosphorylation sites of smooth muscle caldesmon by protein kinase C.

A;Reference number: A44873; MUID:91378498; PMID:1898046

A;Accession: B44873

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <IKE>

A;Experimental source: skeletal myosin

A;Note: sequence extracted from NCBI backbone (NCBIP:63202)

C;Superfamily: caldesmon

Query Match 21.4%; Score 21; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKP 9

||||

Db 8 VEKP 11

RESULT 26

S26664

microtubule-associated protein tau - human

C;Species: Homo sapiens (man)

C;Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995

C;Accession: S26664

R;Andreadis, A.; Brown, W.M.; Kosik, K.S.

Biochemistry 31, 10626-10633, 1992

A;Title: Structure and novel exons of the human tau gene.

A;Reference number: S26662; MUID:93041757; PMID:1420178

A;Accession: S26664

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-18 <AND>
A;Cross-references: EMBL:X61375
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991

Query Match 21.4%; Score 21; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 4.1e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DQPPDVEKPDLO 12
| | :: ||:
Db 8 DHP--LQGPDLR 17

RESULT 27
I57532

gene TnIslow protein - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997
C;Accession: I57532
R;Banerjee-Basu, S.; Buonanno, A.
Mol. Cell. Biol. 13, 7019-7028, 1993
A;Title: cis-acting sequences of the rat troponin I slow gene confer tissue- and development-specific transcription in cultured muscle cells as well as fiber type specificity in transgenic mice.
A;Reference number: I57532; MUID:94019373; PMID:8413291
A;Accession: I57532
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-8 <RES>
A;Cross-references: GB:S66172; NID:g432603
C;Genetics:
A;Gene: TnIslow

Query Match 20.4%; Score 20; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PDVEK 8
|:|:
Db 2 PEVER 6

RESULT 28
A61363

bradykinin - common frog
C;Species: Rana temporaria (common frog)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
C;Accession: A61363
R;Anastasi, A.; Erspamer, V.; Bertaccini, G.
Comp. Biochem. Physiol. A 14, 43-52, 1965
A;Title: Occurrence of bradykinin in the skin of Rana temporaria.
A;Reference number: A61363
A;Accession: A61363
A;Status: preliminary

A;Molecule type: protein
A;Residues: 1-9 <ANA>
C;Superfamily: unassigned animal peptides
C;Keywords: skin

Query Match 20.4%; Score 20; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
| |:
Db 3 PGFSFPR 9

RESULT 29

D48186

ATPase R1 subunit - wood tobacco (fragment)

C;Species: *Nicotiana glauca* (wood tobacco)

C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997

C;Accession: D48186

R;De Paepe, R.; Forchioni, A.; Chetrit, P.; Vedel, F.

Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993

A;Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase beta subunit.

A;Reference number: A48186; MUID:93317598; PMID:8327463

A;Accession: D48186

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9

A;Experimental source: pollen

A;Note: sequence extracted from NCBI backbone (NCBIP:134871)

Query Match 20.4%; Score 20; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 DLQPFQ 15
|| |:
Db 4 DLAPYK 9

RESULT 30

S65433

bradykinin - horn fly (fragment)

C;Species: *Haematobia irritans* (horn fly)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C;Accession: S65433

R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, P.

Eur. J. Biochem. 237, 414-423, 1996

A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran species, *Haematobia irritans exigua*, and its expression in the maturing male reproductive system.

A;Reference number: S65431; MUID:96215437; PMID:8647080

A;Accession: S65433

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <WIJ>
A;Note: the source is designated as *Haematobia irritans exigua*

Query Match 20.4%; Score 20; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
| ||:
Db 3 PGFSPFR 9

RESULT 31

A43065

hydroxyproline-3-bradykinin - frog (*Heleophryne purcelli*)

C;Species: *Heleophryne purcelli*

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999

C;Accession: A43065

R;Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Visser, J.

Experientia 35, 1133, 1979

A;Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the South African leptodactylid frog *Heleophryne purcelli*.

A;Reference number: A43065; MUID:80024576; PMID:488255

A;Accession: A43065

A;Molecule type: protein

A;Residues: 1-9 <NAK>

C;Keywords: bradykinin; hydroxyproline; skin

F;3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
| ||:
Db 3 PGFSPFR 9

RESULT 32

A60476

S-layer protein - *Bacillus thuringiensis* (fragment)

C;Species: *Bacillus thuringiensis*

C;Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 12-Mar-1993

C;Accession: A60476

R;Luckevich, M.D.; Beveridge, T.J.

J. Bacteriol. 171, 6656-6667, 1989

A;Title: Characterization of a dynamic S layer on *Bacillus thuringiensis*.

A;Reference number: A60476; MUID:90078111; PMID:2592346

A;Accession: A60476

A;Molecule type: protein

A;Residues: 1-10 <LUC>

C;Comment: The S-layer, or surface array, is the outermost component of several archaebacteria and eubacteria.

Query Match 20.4%; Score 20; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PDLQP 13
||: |
Db 6 PDVXP 10

RESULT 33

YHRT

morphogenetic neuropeptide - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: A01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator by the authors, because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8
||| |
Db 1 QPPGGSK 7

RESULT 34

YHHU

morphogenetic neuropeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: B01427

A;Molecule type: protein
 A;Residues: 1-11 <BOD>
 R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A;Reference number: A91296; MUID:82050803; PMID:7297679
 A;Contents: annotation; synthesis
 A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.
 C;Superfamily: unassigned animal peptides
 C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
 F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8
 ||| |
 Db 1 QPPGGSK 7

RESULT 35

YHBO

morphogenetic neuropeptide - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: C01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: C01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8
||| |
Db 1 QPPGGSK 7

RESULT 36

YHXA E

morphogenetic neuropeptide - sea anemone (*Anthopleura elegantissima*)

N;Alternate names: head activator

C;Species: *Anthopleura elegantissima*

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: A93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8
||| |
Db 1 QPPGGSK 7

RESULT 37

YHJFHY

morphogenetic neuropeptide - *Hydra attenuata*

N;Alternate names: head activator

C;Species: *Hydra attenuata*

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B93900; A01427
 R;Schaller, H.C.; Bodenmuller, H.
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
 A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
 A;Reference number: A93900
 A;Accession: B93900
 A;Molecule type: protein
 A;Residues: 1-11 <SCH>
 R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A;Reference number: A91296; MUID:82050803; PMID:7297679
 A;Contents: annotation; synthesis
 A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.
 C;Superfamily: unassigned animal peptides
 C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QPPDVEK 8
 ||| |
 Db 1 QPPGGSK 7

RESULT 38 S13279

Ile-Ser-bradykinin - human (fragment)
 N;Alternate names: T-kinin
 C;Species: Homo sapiens (man)
 C;Date: 02-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 24-Jul-1998
 C;Accession: S13279
 R;Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.; Kindermann, G.
 Biol. Chem. Hoppe-Seyler 371, 977-981, 1990
 A;Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human malignant effusions.
 A;Reference number: S13279; MUID:91166748; PMID:2076202
 A;Accession: S13279
 A;Molecule type: protein
 A;Residues: 1-11 <WUN>
 C;Keywords: bradykinin

Query Match 20.4%; Score 20; DB 2; Length 11;
 Best Local Similarity 42.9%; Pred. No. 3.3e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
 | ||:

RESULT 39

C64030

hypothetical protein HI1451 - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 10-Oct-1997

C;Accession: C64030

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: C64030

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-12 <TIGR>

A;Cross-references: GB:U32823; GB:L42023; NID:g1574281; PID:g1574296;

TIGR:HI1451

Query Match 20.4%; Score 20; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPD 5
|||
Db 9 PPD 11

RESULT 40

S15755

actin 7 - soybean (fragment)

C;Species: Glycine max (soybean)

C;Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 13-Aug-1999

C;Accession: S15755

R;Pearson, L.; Meagher, R.B.

Plant Mol. Biol. 14, 513-526, 1990

A;Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated leader: structural similarity to vertebrate muscle actin genes.

A;Reference number: S15754; MUID:91346640; PMID:2102831

A;Accession: S15755

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-13 <PEA>

A;Cross-references: EMBL:X17120; NID:g18527; PIDN:CAA34980.1; PID:g18528

C;Superfamily: actin

C;Keywords: cytoskeleton; structural protein

Query Match 20.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
|:|
Db 6 DIQP 9

RESULT 41

A61361

bradykinin-like peptide - *Bombina orientalis*

C;Species: *Bombina orientalis*

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000

C;Accession: A61361

R;Yasuhara, T.; Hira, M.; Nakajima, T.; Yanaihara, N.; Yanaihara, C.; Hashimoto, T.; Sakura, N.; Tachibana, S.; Araki, K.; Bessho, M.; Yamanaka, T.

Chem. Pharm. Bull. 21, 1388-1391, 1973

A;Title: Active peptides on smooth muscle in the skin of *Bombina orientalis*
Boulenger and characterization of a new bradykinin analogue.

A;Reference number: A61361; MUID:73256822; PMID:4732297

A;Accession: A61361

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <YAS>

C;Superfamily: unassigned animal peptides

C;Keywords: skin

Query Match 20.4%; Score 20; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 4e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
| ||:
Db 3 PGFSPFR 9

RESULT 42

A49155

vasotocin-associated neurophysin - African toad (fragment)

N;Alternate names: MSEL-neurophysin

C;Species: *Bufo regularis* (African toad)

C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2001

C;Accession: A49155

R;Chauvet, J.; Ouedraogo, Y.; Michel, G.; Acher, R.

Comp. Biochem. Physiol. Comp. Physiol. 104, 497-502, 1993

A;Title: Vasotocin and hydrin 2 (vasotocinyl-Gly) in the African toad *Bufo regularis*: study under various environmental conditions.

A;Reference number: A49155; MUID:93230882; PMID:8097151

A;Accession: A49155

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <CHA>

A;Note: sequence extracted from NCBI backbone (NCBIP:129814)

C;Superfamily: oxytocin-neurophysin

C;Keywords: neuropeptide

Query Match 20.4%; Score 20; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 PDVEKPDLQP 13
|| |
Db 3 PDTAVPQCIP 12

RESULT 43

I49407

placental calcium-binding protein - western wild mouse (fragment)

C;Species: Mus spretus (western wild mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999

C;Accession: I49407

R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.;
Nadeau, J.H.

Mamm. Genome 5, 349-355, 1994

A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A;Reference number: I48934; MUID:94319082; PMID:8043949

A;Accession: I49407

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-15 <RES>

A;Cross-references: EMBL:U05696; NID:g497016; PIDN:AAA61936.1; PID:g497017

C;Superfamily: S-100 protein; calmodulin repeat homology

C;Keywords: calcium binding; EF hand

Query Match 20.4%; Score 20; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PDLQP 13
|| :|
Db 8 PDKEP 12

RESULT 44

B39109

hypothetical 1.5K protein - hepatitis C virus

N;Alternate names: hypothetical protein 2

C;Species: hepatitis C virus

C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999

C;Accession: B39109; JQ1585

R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.;
Tekamp-Olson, P.; Kuo, G.; Choo, Q.L.; Houghton, M.
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991

A;Title: Characterization of the terminal regions of hepatitis C viral RNA:
identification of conserved sequences in the 5' untranslated region and poly(A)
tails at the 3' end.

A;Reference number: A39109; MUID:91156678; PMID:1705704

A;Accession: B39109

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-15 <HAN>

A;Cross-references: GB:M58406

R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.

J. Gen. Virol. 73, 1521-1525, 1992

A;Title: Cloning and sequencing of the structural region and expression of putative core gene of hepatitis C virus from a British case of chronic sporadic hepatitis.

A;Reference number: JQ1584; MUID:92300349; PMID:1318944

A;Accession: JQ1585

A;Molecule type: genomic RNA

A;Residues: 1-15 <KUM>

A;Experimental source: strain U.K.

Query Match 20.4%; Score 20; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
||| |
Db 5 QPPGPPLP 12

RESULT 45

F57789

gallbladder stone matrix protein 2, 41K - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 03-May-1996

C;Accession: F57789

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, February 1996

A;Description: The proteins of gallbladder stones.

A;Reference number: A57789

A;Accession: F57789

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <BIN>

A;Note: 9-Phe was also found

Query Match 20.4%; Score 20; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 EKPD 10
:|||
Db 3 DKPD 6

RESULT 46

A61339

vespulakinin 1 - eastern yellowjacket

N;Contains: vespulakinin 2

C;Species: Vespa maculifrons (eastern yellowjacket)

C;Date: 17-Jul-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999

C;Accession: A61339

R;Yoshida, H.; Geller, R.G.; Pisano, J.J.

Biochemistry 15, 61-64, 1976

A;Title: Vespulakinins: new carbohydrate-containing bradykinin derivatives.

A;Reference number: A61339; MUID:76114777; PMID:1247511

A;Accession: A61339

A;Molecule type: protein

A;Residues: 1-17 <YOS>
C;Superfamily: vespulakinin
C;Keywords: antihypertensive; bradykinin; glycoprotein; venom
F;1-17/Product: vespulakinin 1 #status experimental <MAT1>
F;3-17/Product: vespulakinin 2 #status experimental <MAT2>
F;9-17/Region: bradykinin-like
F;3,4/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 20.4%; Score 20; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 5.4e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
| ||:
Db 11 PGFSPFR 17

RESULT 47

B61334

trypsin (EC 3.4.21.4) 2 - starfish (*Dermasterias imbricata*) (fragment)

C;Species: *Dermasterias imbricata*

C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999

C;Accession: B61334

R;Estell, D.A.; Laskowski Jr., M.

Biochemistry 19, 124-131, 1980

A;Title: *Dermasterias imbricata* trypsin 1: an enzyme which rapidly hydrolyzes the reactive-site peptide bonds of protein trypsin inhibitors.

A;Reference number: A61334; MUID:80109692; PMID:7352972

A;Accession: B61334

A;Molecule type: protein

A;Residues: 1-17 <EST>

C;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; protein digestion; serine proteinase

Query Match 20.4%; Score 20; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QPFQV 16
:|:|
Db 12 RPYQV 16

RESULT 48

S15754

actin 6 - soybean (fragment)

C;Species: *Glycine max* (soybean)

C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999

C;Accession: S15754; S08049

R;Pearson, L.; Meagher, R.B.

Plant Mol. Biol. 14, 513-526, 1990

A;Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated leader: structural similarity to vertebrate muscle actin genes.

A;Reference number: S15754; MUID:91346640; PMID:2102831

A;Accession: S15754

A;Molecule type: DNA

A;Residues: 1-17 <PEA>

A;Cross-references: EMBL:X17119; NID:g18525; PIDN:CAA34979.1; PID:g18526
C;Superfamily: actin
C;Keywords: cytoskeleton

Query Match 20.4%; Score 20; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
|:|
Db 6 DIQP 9

RESULT 49

S05033
photosystem II protein psbL - Synechococcus sp. (strain Copeland) (fragment)
N;Alternate names: photosystem II 5K protein
C;Species: Synechococcus sp.
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C;Accession: S05033
R;Ikeuchi, M.; Koike, H.; Inoue, Y.
FEBS Lett. 251, 155-160, 1989
A;Title: Identification of psbI and psbL gene products in cyanobacterial
photosystem II reaction center preparation.
A;Reference number: S05030
A;Accession: S05033
A;Molecule type: protein
A;Residues: 1-17 <IKE>
A;Note: the source is designated as Synechococcus vulcanus
C;Genetics:
A;Gene: psbL
C;Keywords: photosynthesis; photosystem II; thylakoid

Query Match 20.4%; Score 20; DB 2; Length 17;
Best Local Similarity 37.5%; Pred. No. 5.4e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16
|: || ::
Db 5 PNRQPVEL 12

RESULT 50

S59481
hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998
C;Accession: S59481
R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A;Title: Specificity in the immobilisation of cell wall proteins in response to
different elicitor molecules in suspension-cultured cells of French bean
(Phaseolus vulgaris L.).
A;Reference number: S59481; MUID:96011753; PMID:7548825
A;Accession: S59481
A;Molecule type: protein
A;Residues: 1-17 <WOJ>

C;Keywords: glycoprotein; hydroxyproline

F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 20.4%; Score 20; DB 2; Length 17;

Best Local Similarity 57.1%; Pred. No. 5.4e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKP 9

|| | |

Db 9 PPPVVYP 15

Search completed: July 4, 2004, 04:47:15

Job time : 14.8358 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:45:52 ; Search time 35.3284 Seconds
(without alignments)
158.601 Million cell updates/sec

Title: US-09-641-802-3
Perfect score: 98
Sequence: 1 DQPPDVEKPDLPFQVQS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 203405

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	98	100.0	18	14	US-10-281-652-3	Sequence 3, Appli
2	41	41.8	15	12	US-10-014-340-759	Sequence 759, App
3	39	39.8	16	14	US-10-225-567A-1755	Sequence 1755, Ap
4	35	35.7	12	12	US-10-014-340-526	Sequence 526, App
5	32	32.7	9	14	US-10-350-258-6	Sequence 6, Appli
6	32	32.7	18	14	US-10-161-791-305	Sequence 305, App
7	31	31.6	10	10	US-09-572-404B-3283	Sequence 3283, Ap
8	31	31.6	11	12	US-10-601-837-34	Sequence 34, Appl
9	30	30.6	11	14	US-10-022-066-144	Sequence 144, App
10	30	30.6	11	14	US-10-022-066-374	Sequence 374, App
11	30	30.6	15	15	US-10-149-138-3845	Sequence 3845, Ap
12	30	30.6	15	16	US-10-149-138-3845	Sequence 3845, Ap
13	29	29.6	8	12	US-09-891-823-98	Sequence 98, Appl
14	29	29.6	8	14	US-10-365-908-98	Sequence 98, Appl
15	29	29.6	9	14	US-10-033-662-36	Sequence 36, Appl
16	29	29.6	10	10	US-09-572-404B-3027	Sequence 3027, Ap
17	29	29.6	13	10	US-09-992-665-47	Sequence 47, Appl
18	29	29.6	15	14	US-10-080-608A-70	Sequence 70, Appl
19	29	29.6	15	15	US-10-370-685-159	Sequence 159, App
20	29	29.6	15	15	US-10-371-067-1	Sequence 1, Appli
21	29	29.6	17	14	US-10-225-567A-1370	Sequence 1370, Ap
22	29	29.6	17	16	US-10-443-349-12	Sequence 12, Appl
23	29	29.6	18	9	US-09-922-261-200	Sequence 200, App
24	28	28.6	9	15	US-10-107-532-25	Sequence 25, Appl
25	28	28.6	9	15	US-10-107-532-652	Sequence 652, App
26	28	28.6	9	15	US-10-107-532-2214	Sequence 2214, Ap
27	28	28.6	9	15	US-10-107-532-2776	Sequence 2776, Ap
28	28	28.6	9	15	US-10-107-532-3286	Sequence 3286, Ap
29	28	28.6	9	15	US-10-107-532-3991	Sequence 3991, Ap
30	28	28.6	10	15	US-10-107-532-284	Sequence 284, App
31	28	28.6	10	15	US-10-107-532-896	Sequence 896, App
32	28	28.6	10	15	US-10-107-532-1418	Sequence 1418, Ap
33	28	28.6	10	15	US-10-107-532-1923	Sequence 1923, Ap
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36	28	28.6	10	15	US-10-107-532-4968	Sequence 4968, Ap
37	28	28.6	10	15	US-10-107-532-5105	Sequence 5105, Ap
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39	28	28.6	12	12	US-10-609-217-673	Sequence 673, App
40	28	28.6	12	12	US-10-609-217-683	Sequence 683, App
41	28	28.6	12	12	US-10-609-217-958	Sequence 958, App
42	28	28.6	12	12	US-10-632-388-673	Sequence 673, App
43	28	28.6	12	12	US-10-632-388-683	Sequence 683, App
44	28	28.6	12	12	US-10-632-388-958	Sequence 958, App
45	28	28.6	12	12	US-10-651-723-673	Sequence 673, App
46	28	28.6	12	12	US-10-651-723-683	Sequence 683, App
47	28	28.6	12	12	US-10-651-723-958	Sequence 958, App
48	28	28.6	12	12	US-10-645-761-673	Sequence 673, App
49	28	28.6	12	12	US-10-645-761-683	Sequence 683, App
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51	28	28.6	12	16	US-10-666-696-673	Sequence 673, App
52	28	28.6	12	16	US-10-666-696-683	Sequence 683, App
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54	28	28.6	12	16	US-10-653-048-673	Sequence 673, App
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56	28	28.6	12	16	US-10-653-048-958	Sequence 958, App

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59	28	28.6	15	16	US-10-647-005-53	Sequence 53, Appl
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89	28	28.6	17	16	US-10-653-048-847	Sequence 847, App
90	28	28.6	17	16	US-10-653-048-848	Sequence 848, App
91	27	27.6	9	8	US-08-344-824-162	Sequence 162, App
92	27	27.6	9	12	US-09-891-823-122	Sequence 122, App
93	27	27.6	9	14	US-10-365-908-122	Sequence 122, App
94	27	27.6	9	14	US-10-357-175-148	Sequence 148, App
95	27	27.6	9	15	US-10-455-720-148	Sequence 148, App
96	27	27.6	9	15	US-10-149-138-4079	Sequence 4079, Ap
97	27	27.6	9	16	US-10-149-138-4079	Sequence 4079, Ap
98	27	27.6	10	8	US-08-344-824-251	Sequence 251, App
99	27	27.6	10	12	US-09-891-823-114	Sequence 114, App
100	27	27.6	10	12	US-10-601-100-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
 US-10-281-652-3
 ; Sequence 3, Application US/10281652
 ; Publication No. US20030091606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan

```
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-3
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Query Match          100.0%; Score 98; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 DQPPDVEKPDLPFQVQS 18
        |||||
Db      1 DQPPDVEKPDLPFQVQS 18
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RESULT 2

US-10-014-340-759

```
; Sequence 759, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor,
Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 759
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-759
```

```
Query Match          41.8%; Score 41; DB 12; Length 15;
Best Local Similarity 47.1%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches 0; Indels 6; Gaps 1;
```

```
Qy      1 DQPPDVEKPDLPFQVQ 17
        |||||:|      ||::
Db      5 DQPPDIE-----FQIR 15
```

RESULT 3 .

US-10-225-567A-1755

; Sequence 1755, Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LifeSpan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Burmer, Glenna C.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
 RECEPTORS (GPCRS)
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1755
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-225-567A-1755

Query Match 39.8%; Score 39; DB 14; Length 16;
 Best Local Similarity 50.0%; Pred. No. 55;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLP 13
 :|||: | | |
 Db 5 RPPDIRKSDSSP 16

RESULT 4

US-10-014-340-526

; Sequence 526, Application US/10014340
 ; Publication No. US20030064411A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Herath, et al
 ; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor,
 Including
 ; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
 ; FILE REFERENCE: 9195-078
 ; CURRENT APPLICATION NUMBER: US/10/014,340
 ; CURRENT FILING DATE: 2001-12-10
 ; NUMBER OF SEQ ID NOS: 823
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 526
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-014-340-526

Query Match 35.7%; Score 35; DB 12; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKPD LQ 12
|| | ||:
Db 3 PPSAEY PDLR 12

RESULT 5

US-10-350-258-6

; Sequence 6, Application US/10350258
; Publication No. US20030139345A1
; GENERAL INFORMATION:
; APPLICANT: MATTHIAS RATH
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND METHODS FOR TREATING CANCER
INVASION AND METASTASIS
; FILE REFERENCE: 11957/23
; CURRENT APPLICATION NUMBER: US/10/350,258
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/351,317
; PRIOR FILING DATE: January 23, 2002
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-350-258-6

Query Match 32.7%; Score 32; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPDVEKPD 10
||||: |
Db 2 PPDVQRVD 9

RESULT 6

US-10-161-791-305

; Sequence 305, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

```

; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-305

```

```

Query Match          32.7%; Score 32; DB 14; Length 18;
Best Local Similarity 43.8%; Pred. No. 6.4e+02;
Matches      7; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

Qy      2 QPPDVEKPDLPFQVQ 17
        |||  |  ||  |
Db      3 QPPYFPPPPYQPIYPQ 18

```

RESULT 7

```

US-09-572-404B-3283
; Sequence 3283, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3283
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 291-300 and may
interact with.

```

; OTHER INFORMATION: Sequence 3284 in this patent.
US-09-572-404B-3283

Query Match 31.6%; Score 31; DB 10; Length 10;
Best Local Similarity 71.4%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPDVEKP 9
|||:|
Db 3 PPTVQKP 9

RESULT 8

US-10-601-837-34
; Sequence 34, Application US/10601837
; Publication No. US20040053309A1
; GENERAL INFORMATION:
; APPLICANT: Holt, Gordon D
; APPLICANT: Kelly, Michael D
; APPLICANT: Kennedy, Sandra J
; APPLICANT: Moyses, Christopher
; TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment
of Kidney
; TITLE OF INVENTION: Response
; FILE REFERENCE: 2543-1-030
; CURRENT APPLICATION NUMBER: US/10/601,837
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: PCT/GB01/05777
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: US 60/260392
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Ratus No. US20040053309Alvegicus
US-10-601-837-34

Query Match 31.6%; Score 31; DB 12; Length 11;
Best Local Similarity 55.6%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 EKPDLPFFQ 15
:|:| |||
Db 2 DNPNLPPFQ 10

RESULT 9

US-10-022-066-144
; Sequence 144, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF

```

; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Unknown amino acid
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (3)
;   OTHER INFORMATION: Unknown amino acid
US-10-022-066-144

```

```

Query Match          30.6%;  Score 30;  DB 14;  Length 11;
Best Local Similarity 57.1%;  Pred. No. 7.3e+02;
Matches      4;  Conservative    2;  Mismatches    1;  Indels      0;  Gaps      0;

```

```

Qy      1 DQPPDVE 7
        | |||::
Db      4 DPPPDMZ 10

```

RESULT 10

```

US-10-022-066-374
; Sequence 374, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17

```


; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 374
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Unknown amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3)
; OTHER INFORMATION: Unknown amino acid
US-10-022-066-374

Query Match 30.6%; Score 30; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 7.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQPPDVE 7
| |||::
Db 4 DPPPDMZ 10

RESULT 11
US-10-149-138-3845
; Sequence 3845, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3845
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3845

Query Match 30.6%; Score 30; DB 15; Length 15;
Best Local Similarity 45.5%; Pred. No. 1e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLP 13
| | :||::|
Db 1 PEYVNQPDVRP 11

RESULT 12

US-10-149-138-3845

; Sequence 3845, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3845
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3845

Query Match 30.6%; Score 30; DB 16; Length 15;
Best Local Similarity 45.5%; Pred. No. 1e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLP 13
| | :||::|
Db 1 PEYVNQPDVRP 11

RESULT 13

US-09-891-823-98

; Sequence 98, Application US/09891823
; Publication No. US20020110566A1

```
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Human papilloma virus
US-09-891-823-98
```

```
Query Match          29.6%; Score 29; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      2 QPPDV 6
        |||||
Db      2 QPPDV 6
```

```
RESULT 14
US-10-365-908-98
; Sequence 98, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Human papilloma virus
US-10-365-908-98
```

```
Query Match          29.6%; Score 29; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPDV 6
|||||
Db 2 QPPDV 6

RESULT 15

US-10-033-662-36

; Sequence 36, Application US/10033662
; Publication No. US20030092197A1
; GENERAL INFORMATION:
; APPLICANT: Herman, et al.
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment
of Cardiac
; TITLE OF INVENTION: Response
; FILE REFERENCE: 9195-081
; CURRENT APPLICATION NUMBER: US/10/033,662
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-662-36

Query Match 29.6%; Score 29; DB 14; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 KPDLQP 13
|||||
Db 1 KPDLSP 6

RESULT 16

US-09-572-404B-3027

; Sequence 3027, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3027
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in GUCY2D OR GUC2D OR RETGC1 OR RETGC OR
GUC1A4 OR
; OTHER INFORMATION: CORD6 at 1069-1078 and may interact with Sequence 3028 in
this patent.

US-09-572-404B-3027

Query Match 29.6%; Score 29; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13
|||||
Db 2 PDLQP 6

RESULT 17

US-09-992-665-47

; Sequence 47, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-47

Query Match 29.6%; Score 29; DB 10; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QPPDVEKPDLQP 13
||| : | |
Db 1 QPPSMSSPPPPP 12

RESULT 18

US-10-080-608A-70

; Sequence 70, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 70
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human rhinovirus 2
US-10-080-608A-70

Query Match 29.6%; Score 29; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13
|||||
Db 9 PDLQP 13

RESULT 19

US-10-370-685-159

; Sequence 159, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional
Elements
; FILE REFERENCE: NANF.P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human rhinovirus 2
US-10-370-685-159

Query Match 29.6%; Score 29; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PDLQP 13
|||||
Db 9 PDLQP 13

RESULT 20

US-10-371-067-1

; Sequence 1, Application US/10371067
; Publication No. US20040018587A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Williams, Mark K
; APPLICANT: Goldberg, Edward B
; TITLE OF INVENTION: Nanostructures containing antibody assembly subunits
; FILE REFERENCE: NANF.P-003
; CURRENT APPLICATION NUMBER: US/10/371,067

```
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/136,225
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/236,949
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/542,003
; PRIOR FILING DATE: 1995-10-12
; PRIOR APPLICATION NUMBER: 08/322,760
; PRIOR FILING DATE: 1994-10-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: (Antibody 8F5) Complexed With Peptide From Human
Rhinovirus
; OTHER INFORMATION: (Serotype 2) Viral Capsid Protein Vp2 (Residues 156 -170)
US-10-371-067-1
```

```
Query Match          29.6%; Score 29; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      9 PDLQP 13
        |||||
Db      9 PDLQP 13
```

RESULT 21

```
US-10-225-567A-1370
; Sequence 1370, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1370
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1370
```

```
Query Match          29.6%; Score 29; DB 14; Length 17;
```

Best Local Similarity 41.7%; Pred. No. 1.6e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 7 EKPDLQPFQVQS 18
: |||| :: |
Db 6 KNPDLQAIRIAS 17

RESULT 22

US-10-443-349-12

; Sequence 12, Application US/10443349
; Publication No. US20040023856A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert E.
; APPLICANT: Wagman, David W.
; TITLE OF INVENTION: Blk CHAIN OF LAMININ AND METHODS OF USE
; FILE REFERENCE: 10287/021003
; CURRENT APPLICATION NUMBER: US/10/443,349
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US/09/161,872
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 08/735,893
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-443-349-12

Query Match 29.6%; Score 29; DB 16; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPD 10
|: ||:| |
Db 1 DENPDIECAD 10

RESULT 23

US-09-922-261-200

; Sequence 200, Application US/09922261
; Patent No. US20020111471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES
INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999

; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-261-200

Query Match 29.6%; Score 29; DB 9; Length 18;
Best Local Similarity 54.5%; Pred. No. 1.7e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 VEKPDLPFFQV 16
: ||| || |:
Db 1 MEKPKLQRHQL 11

RESULT 24

US-10-107-532-25

; Sequence 25, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-25

Query Match 28.6%; Score 28; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||
Db 1 QPEPLEKP 8

RESULT 25

US-10-107-532-652

; Sequence 652, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 652
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-652

Query Match 28.6%; Score 28; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||
Db 2 QPEPLEKP 9

RESULT 26

US-10-107-532-2214

; Sequence 2214, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Morrison, Robert Kendall
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Afar, Daniel E.H.
 ; APPLICANT: Ge, Wangmao
 ; APPLICANT: Raitano, Arthur
 ; APPLICANT: Challita-Eid, Pia M.
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
 Cancer
 ; FILE REFERENCE: 51158-200064.00
 ; CURRENT APPLICATION NUMBER: US/10/107,532
 ; CURRENT FILING DATE: 2002-08-05
 ; PRIOR APPLICATION NUMBER: 60/283,112
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/286,630
 ; PRIOR FILING DATE: 2001-04-25
 ; NUMBER OF SEQ ID NOS: 6321
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2214
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-107-532-2214

Query Match 28.6%; Score 28; DB 15; Length 9;
 Best Local Similarity 62.5%; Pred. No. 1.2e+06;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
 || :|||
 Db 1 QPEPLEKP 8

RESULT 27
 US-10-107-532-2776
 ; Sequence 2776, Application US/10107532
 ; Publication No. US20040003418A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Jakobovits, Aya
 ; APPLICANT: Faris, Mary
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Morrison, Robert Kendall
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Afar, Daniel E.H.
 ; APPLICANT: Ge, Wangmao
 ; APPLICANT: Raitano, Arthur
 ; APPLICANT: Challita-Eid, Pia M.
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
 Cancer
 ; FILE REFERENCE: 51158-200064.00
 ; CURRENT APPLICATION NUMBER: US/10/107,532
 ; CURRENT FILING DATE: 2002-08-05
 ; PRIOR APPLICATION NUMBER: 60/283,112
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/286,630

; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2776
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-2776

Query Match 28.6%; Score 28; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||
Db 1 QPEPLEKP 8

RESULT 28

US-10-107-532-3286
; Sequence 3286, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3286
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-3286

Query Match 28.6%; Score 28; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||

Db 1 QPEPLEKP 8

RESULT 29

US-10-107-532-3991

; Sequence 3991, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3991
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-3991

Query Match 28.6%; Score 28; DB 15; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||
Db 1 QPEPLEKP 8

RESULT 30

US-10-107-532-284

; Sequence 284, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.

```
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-284
```

```
Query Match      28.6%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches      5; Conservative      1; Mismatches      2; Indels      0; Gaps      0;
```

```
Qy      2 QPPDVEKP 9
      || :|||
Db      1 QPEPLEKP 8
```

RESULT 31

```
US-10-107-532-896
; Sequence 896, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
```

; SEQ ID NO 896
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-896

Query Match 28.6%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||
Db 2 QPEPLEKP 9

RESULT 32

US-10-107-532-1418

; Sequence 1418, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1418
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-1418

Query Match 28.6%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||
Db 1 QPEPLEKP 8

RESULT 33

US-10-107-532-1923

; Sequence 1923, Application US/10107532
 ; Publication No. US20040003418A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Jakobovits, Aya
 ; APPLICANT: Faris, Mary
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Morrison, Robert Kendall
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Afar, Daniel E.H.
 ; APPLICANT: Ge, Wangmao
 ; APPLICANT: Raitano, Arthur
 ; APPLICANT: Challita-Eid, Pia M.
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 ; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
 Cancer
 ; FILE REFERENCE: 51158-200064.00
 ; CURRENT APPLICATION NUMBER: US/10/107,532
 ; CURRENT FILING DATE: 2002-08-05
 ; PRIOR APPLICATION NUMBER: 60/283,112
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/286,630
 ; PRIOR FILING DATE: 2001-04-25
 ; NUMBER OF SEQ ID NOS: 6321
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1923
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-107-532-1923

Query Match 28.6%; Score 28; DB 15; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.3e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
 || :|||
 Db 1 QPEPLEKP 8

RESULT 34

US-10-107-532-2499

; Sequence 2499, Application US/10107532
 ; Publication No. US20040003418A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Jakobovits, Aya
 ; APPLICANT: Faris, Mary
 ; APPLICANT: Morrison, Karen Jane Meyrick
 ; APPLICANT: Morrison, Robert Kendall
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Afar, Daniel E.H.
 ; APPLICANT: Ge, Wangmao
 ; APPLICANT: Raitano, Arthur
 ; APPLICANT: Challita-Eid, Pia M.

; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2499
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-2499

Query Match 28.6%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||
Db 2 QPEPLEKP 9

RESULT 35

US-10-107-532-3566

; Sequence 3566, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3566
; LENGTH: 10
; TYPE: PRT

; ORGANISM: Homo sapien
US-10-107-532-3566

Query Match 28.6%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||
Db 2 QPEPLEKP 9

RESULT 36

US-10-107-532-4968

; Sequence 4968, Application US/10107532

; Publication No. US20040003418A1

; GENERAL INFORMATION:

; APPLICANT: Agensys, Inc.

; APPLICANT: Jakobovits, Aya

; APPLICANT: Faris, Mary

; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Morrison, Robert Kendall

; APPLICANT: Hubert, Rene S.

; APPLICANT: Afar, Daniel E.H.

; APPLICANT: Ge, Wangmao

; APPLICANT: Raitano, Arthur

; APPLICANT: Challita-Eid, Pia M.

; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer

; FILE REFERENCE: 51158-200064.00

; CURRENT APPLICATION NUMBER: US/10/107,532

; CURRENT FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: 60/283,112

; PRIOR FILING DATE: 2001-04-10

; PRIOR APPLICATION NUMBER: 60/286,630

; PRIOR FILING DATE: 2001-04-25

; NUMBER OF SEQ ID NOS: 6321

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4968

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-107-532-4968

Query Match 28.6%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
|| :|||
Db 1 QPEPLEKP 8

RESULT 37

US-10-107-532-5105

; Sequence 5105, Application US/10107532

```

; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Arthur
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 158P3D2 Useful in Treatment and Detection of
Cancer
; FILE REFERENCE: 51158-200064.00
; CURRENT APPLICATION NUMBER: US/10/107,532
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5105
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-5105

```

```

Query Match          28.6%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches      5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      2 QPPDVEKP 9
        || :|||
Db      1 QPEPLEKP 8

```

```

RESULT 38
US-09-906-393A-9
; Sequence 9, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT

```

; ORGANISM: Homo sapiens
US-09-906-393A-9

Query Match 28.6%; Score 28; DB 10; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PDVEKPD 10
|| :||:
Db 1 PDAKKPE 7

RESULT 39

US-10-609-217-673
; Sequence 673, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-609-217-673

Query Match 28.6%; Score 28; DB 12; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 40

US-10-609-217-683
; Sequence 683, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES

```
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 683
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-609-217-683
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Query Match          28.6%; Score 28; DB 12; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches      5; Conservative      1; Mismatches      1; Indels      0; Gaps      0;
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Qy      12 QPFQVQS 18
        ||: |||
Db      6 QPYSVQS 12
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RESULT 41
US-10-609-217-958
; Sequence 958, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 958
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: Position 5, Xaa = naphthylalanine
US-10-609-217-958
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Query Match 28.6%; Score 28; DB 12; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 42

US-10-632-388-673
; Sequence 673, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-632-388-673

Query Match 28.6%; Score 28; DB 12; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 43

US-10-632-388-683
; Sequence 683, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527

; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 683
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-632-388-683

Query Match 28.6%; Score 28; DB 12; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 44

US-10-632-388-958
; Sequence 958, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 958
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: Position 5, Xaa = naphthylalanine
US-10-632-388-958

Query Match 28.6%; Score 28; DB 12; Length 12;

Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 45

US-10-651-723-673

; Sequence 673, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-651-723-673

Query Match 28.6%; Score 28; DB 12; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 46

US-10-651-723-683

; Sequence 683, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 683
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-651-723-683

Query Match 28.6%; Score 28; DB 12; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 47

US-10-651-723-958

; Sequence 958, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 958
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: Position 5, Xaa = naphthylalanine
US-10-651-723-958

Query Match 28.6%; Score 28; DB 12; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 48

US-10-645-761-673

; Sequence 673, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-645-761-673

Query Match 28.6%; Score 28; DB 12; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 49

US-10-645-761-683

; Sequence 683, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22

; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 683
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-645-761-683

Query Match 28.6%; Score 28; DB 12; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18
||: |||
Db 6 QPYSVQS 12

RESULT 50

US-10-645-761-958
; Sequence 958, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 958
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: Position 5, Xaa = naphthylalanine
US-10-645-761-958

Query Match 28.6%; Score 28; DB 12; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 QPFQVQS 18

Db ||: |||
 6 QPYSVQS 12

Search completed: July 4, 2004, 05:12:24
Job time : 36.3284 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:51 ; Search time 30.6269 Seconds
(without alignments)
185.436 Million cell updates/sec

Title: US-09-641-802-3
Perfect score: 98
Sequence: 1 DQPPDVEKPDLPFQVQS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 5664

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result Query
No. Score Match Length DB ID Description

1	31	31.6	18	6	P82674	P82674 bos taurus
2	29	29.6	15	8	Q9T2K8	Q9t2k8 spinacia ol
3	29	29.6	17	15	Q8UT86	Q8ut86 human immun
4	28.5	29.1	17	4	Q9UDD6	Q9udd6 homo sapien
5	28	28.6	18	2	Q9R4E0	Q9r4e0 pseudomonas
6	28	28.6	18	13	O13167	O13167 xiphias gla
7	27	27.6	10	13	Q9PRY8	Q9pry8 triakis scy
8	27	27.6	12	10	P82325	P82325 pisum sativ
9	27	27.6	16	4	Q9UCI2	Q9uci2 homo sapien
10	27	27.6	18	5	Q8MNX0	Q8mnx0 bombyx mori
11	27	27.6	18	10	Q9S8G8	Q9s8g8 psophocarpu
12	26	26.5	13	4	Q9UEE2	Q9uee2 homo sapien
13	26	26.5	15	1	Q9UWH3	Q9uwh3 thermococcu
14	26	26.5	15	6	Q9TR14	Q9tr14 bos taurus
15	26	26.5	17	11	Q9JK08	Q9jk08 mus musculu
16	26	26.5	17	15	P90402	P90402 human immun
17	26	26.5	17	15	Q9Q709	Q9q709 human immun
18	26	26.5	18	2	Q9X3E9	Q9x3e9 prochloroco
19	26	26.5	18	5	Q9TWL5	Q9twl5 lucilia cup
20	25.5	26.0	17	10	P83061	P83061 spinacia ol
21	25	25.5	18	4	Q9UCT9	Q9uct9 homo sapien
22	24	24.5	11	2	Q9S618	Q9s618 prochloroco
23	24	24.5	12	10	P82328	P82328 pisum sativ
24	24	24.5	13	2	Q9R3R6	Q9r3r6 prochloroco
25	24	24.5	17	2	Q9LB06	Q9lb06 prochloroco
26	24	24.5	18	2	O67971	O67971 synechococc
27	23.5	24.0	9	4	Q9UCS8	Q9ucs8 homo sapien
28	23	23.5	9	2	Q9R735	Q9r735 streptomyce
29	23	23.5	14	2	P81715	P81715 streptomyce
30	23	23.5	17	2	P97135	P97135 mycobacteri
31	23	23.5	18	8	Q7YMC5	Q7ymc5 pogonatum s
32	22	22.4	10	2	Q9L5W6	Q9l5w6 liberibacte
33	22	22.4	11	6	Q8HYM4	Q8hym4 felis silve
34	22	22.4	14	11	Q9RLU3	Q9rlu3 rattus norv
35	22	22.4	15	2	O69142	O69142 streptococc
36	22	22.4	15	10	Q08936	Q08936 nicotiana t
37	22	22.4	16	11	Q9QVL2	Q9qvl2 mus sp. mep
38	22	22.4	17	2	Q9EUP4	Q9eup4 thermus the
39	22	22.4	17	6	O46667	O46667 macropus ro
40	22	22.4	17	6	Q95M99	Q95m99 equus cabal
41	22	22.4	17	11	Q9QVC6	Q9qvc6 rattus norv
42	22	22.4	17	11	Q9QVC2	Q9qvc2 rattus sp.
43	22	22.4	17	12	Q919B0	Q919b0 human papil
44	22	22.4	18	2	Q56610	Q56610 vibrio chol
45	22	22.4	18	4	Q9P0M3	Q9p0m3 homo sapien
46	22	22.4	18	4	Q96C65	Q96c65 homo sapien
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48	22	22.4	18	12	Q919D5	Q919d5 human papil
49	22	22.4	18	12	Q919B3	Q919b3 human papil
50	22	22.4	18	12	Q919B5	Q919b5 human papil
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52	22	22.4	18	12	Q919C5	Q919c5 human papil
53	22	22.4	18	12	Q919D1	Q919d1 human papil
54	22	22.4	18	12	Q919D3	Q919d3 human papil
55	22	22.4	18	12	Q919B9	Q919b9 human papil
56	22	22.4	18	12	Q919A8	Q919a8 human papil
57	22	22.4	18	12	Q919C7	Q919c7 human papil

58	22	22.4	18	12	Q919C9	Q919c9 human papil
59	21.5	21.9	17	6	Q95KQ7	Q95kq7 sus scrofa
60	21	21.4	9	10	P82429	P82429 nicotiana t
61	21	21.4	10	8	Q8SHA8	Q8sha8 rhampholeon
62	21	21.4	13	6	Q9TQS4	Q9tqs4 equus cabal
63	21	21.4	13	6	Q865C9	Q865c9 sus scrofa
64	21	21.4	13	8	Q9T2U1	Q9t2u1 bos taurus
65	21	21.4	14	5	Q26075	Q26075 psammechinu
66	21	21.4	14	11	Q9JJU5	Q9jju5 mus musculu
67	21	21.4	16	2	Q9R596	Q9r596 micrococcus
68	21	21.4	16	8	Q8HU27	Q8hu27 passiflora
69	21	21.4	16	8	Q8HU26	Q8hu26 passiflora
70	21	21.4	16	11	Q9QUW5	Q9quw5 rattus sp.
71	21	21.4	16	11	Q9QUW8	Q9quw8 cavia (guin
72	21	21.4	17	2	Q8VME2	Q8vme2 pseudomonas
73	21	21.4	17	6	Q9TRW1	Q9trw1 oryctolagus
74	21	21.4	18	6	Q9TT81	Q9tt81 bos taurus
75	21	21.4	18	11	Q9QZX4	Q9qzx4 mus spretus
76	21	21.4	18	11	Q9QZX5	Q9qzx5 mus musculu
77	20	20.4	8	11	Q80XV8	Q80xv8 rattus sp.
78	20	20.4	9	4	Q16605	Q16605 homo sapien
79	20	20.4	10	11	Q63056	Q63056 rattus norv
80	20	20.4	13	11	Q9QVL4	Q9qvl4 rattus sp.
81	20	20.4	13	11	O88176	O88176 mus musculu
82	20	20.4	15	2	Q9KIV5	Q9kiv5 anabaena sp
83	20	20.4	15	5	Q9TWT4	Q9twt4 lumbricus t
84	20	20.4	15	10	Q9AT15	Q9at15 lycopersico
85	20	20.4	15	10	P82431	P82431 nicotiana t
86	20	20.4	15	11	Q62531	Q62531 mus spretus
87	20	20.4	15	11	Q8CJ29	Q8cj29 mus musculu
88	20	20.4	16	5	Q9TWN7	Q9tnw7 toxoplasma
89	20	20.4	16	6	Q9TR97	Q9tr97 oryctolagus
90	20	20.4	17	4	Q16231	Q16231 homo sapien
91	20	20.4	17	4	Q9UEJ5	Q9uej5 homo sapien
92	20	20.4	17	5	Q9TWB9	Q9twb9 acanthamoeb
93	20	20.4	17	8	Q85UP3	Q85up3 acrocladium
94	20	20.4	17	8	Q7YMZ4	Q7ymz4 porothamniu
95	20	20.4	17	8	Q7YMZ1	Q7ymz1 porotrichum
96	20	20.4	17	11	Q9QVK3	Q9qvk3 rattus sp.
97	20	20.4	18	2	Q8VNJ9	Q8vnj9 haemophilus
98	20	20.4	18	2	Q9R5B0	Q9r5b0 arthrobacte
99	20	20.4	18	4	Q8NFB4	Q8nfb4 homo sapien
100	20	20.4	18	6	Q9TQR9	Q9tqr9 mammuthus p

ALIGNMENTS

RESULT 1

P82674

ID P82674 PRELIMINARY; PRT; 18 AA.

AC P82674;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Mitochondrial 28S ribosomal protein S5 (MRP-S5) (Fragments).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Liver;
 RA Koc E.C., Burkhart W., Blackburn K., Moseley A., Koc H.,
 RA Spremulli L.L.;
 RT "Identification of four proteins from the small subunit of the
 RT mammalian mitochondrial ribosome using a proteomics approach.";
 RL Submitted (JUL-2000) to Swiss-Prot.
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -!- MASS SPECTROMETRY: MW=974.58; METHOD=ELECTROSPRAY; RANGE=1-8.
 CC -!- SIMILARITY: BELONGS TO THE S5P FAMILY OF RIBOSOMAL PROTEINS.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR InterPro; IPR000851; Ribosomal_S5.
 DR PROSITE; PS00585; RIBOSOMAL_S5; PARTIAL.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1 1
 FT NON_CONS 8 9
 FT UNSURE 17 17 OR I.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2127 MW; 199BC913E7E25FAF CRC64;

Query Match 31.6%; Score 31; DB 6; Length 18;
 Best Local Similarity 66.7%; Pred. No. 4.5e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PDVEKPDQLQ 12
 | : | ||||
 Db 10 PEDEVPDQLQ 18

RESULT 2

Q9T2K8

ID Q9T2K8 PRELIMINARY; PRT; 15 AA.
 AC Q9T2K8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE LHCII kinase, 64 kDa kinase (Fragment).
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Amaranthaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92183823; PubMed=1544419;
 RA Gal A., Herrmann R.G., Lottspeich F., Ohad I.;
 RT "Phosphorylation of cytochrome b6 by the LHC II kinase associated with
 RT the cytochrome complex.";
 RL FEBS Lett. 298:33-35(1992).
 DR PIR; S20410; S20410.

DR PIR; S66419; S66419.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1556 MW; 6E00A4F917DDF33E CRC64;

Query Match 29.6%; Score 29; DB 8; Length 15;
Best Local Similarity 75.0%; Pred. No. 7.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PDVEKPD L 11
| | | | | |
Db 5 PDVEKSTL 12

RESULT 3

Q8UT86

ID Q8UT86 PRELIMINARY; PRT; 17 AA.
AC Q8UT86;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein.
GN VPR.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=00BW1795.6;
RA Novitsky V.A., Smith U.R., Gilbert P., McLane M.F., Chigwedere P.,
RA Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., Thior I.,
RA Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannberg F.,
RA Marlink R., Lee T.-H., Essex M.;
RT "HIV-1 subtype C molecular phylogeny: consensus sequence for an AIDS
RT vaccine design.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF443097; AAL34763.1; -.
DR InterPro; IPR000012; RetroV_Vpr/X.
DR Pfam; PF00522; VPR; 1.
KW AIDS.
SQ SEQUENCE 17 AA; 2018 MW; 58CA6A463F4457C7 CRC64;

Query Match 29.6%; Score 29; DB 15; Length 17;
Best Local Similarity 28.6%; Pred. No. 8.7e+02;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPD LQPF 14
: | | : | : | :
Db 2 EQAPEDQGPQREPY 15

RESULT 4

Q9UDD6

ID Q9UDD6 PRELIMINARY; PRT; 17 AA.
AC Q9UDD6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fatty acid ETHYL ester synthase-II, FAEE synthase-II (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92317032; PubMed=1618826;
 RA Bora P.S., Wu X., Spilburg C.A., Lange L.G.;
 RT "Purification and characterization of fatty acid ethyl ester synthase-
 RT II from human myocardium."
 RL J. Biol. Chem. 267:13217-13221(1992).
 DR PIR; A42920; A42920.
 DR GO; GO:0005829; C:cytosol; NAS.
 DR GO; GO:0030339; F:fatty-acyl-ethyl-ester synthase activity; NAS.
 DR GO; GO:0006067; P:ethanol metabolism; NAS.
 DR GO; GO:0006631; P:fatty acid metabolism; NAS.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1755 MW; 3456973BF1B39273 CRC64;

Query Match 29.1%; Score 28.5; DB 4; Length 17;
 Best Local Similarity 46.2%; Pred. No. 1e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 1 DQPPDVEKPDLQP 13
 : ||| || |
 Db 1 EDPPD---PDTP 10

RESULT 5

Q9R4E0

ID Q9R4E0 PRELIMINARY; PRT; 18 AA.
 AC Q9R4E0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Dipeptidyl aminopeptidase type I (Fragment).
 OS Pseudomonas.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae.
 OX NCBI_TaxID=286;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96200096; PubMed=8631703;
 RA Ogasawara W., Ochiai K., Ando K., Yano K., Yamasaki M., Okada H.,
 RA Morikawa Y.;
 RT "A novel dipeptidyl aminopeptidase from Pseudomonas sp. strain WO24."
 RL J. Bacteriol. 178:1283-1288(1996).
 SQ SEQUENCE 18 AA; 1813 MW; 369B0388C394A737 CRC64;

Query Match 28.6%; Score 28; DB 2; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPDVEK 8

Db | | | | |
5 PPDVAK 10

RESULT 6

O13167

ID O13167 PRELIMINARY; PRT; 18 AA.
AC O13167;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein S7 (Fragment).
OS Xiphias gladius (Swordfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Xiphiidae; Xiphias.
OX NCBI_TaxID=8245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Chow S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=J26B;
RA Chow S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U95521; AAB58281.1; -.
DR EMBL; U89244; AAB58379.1; -.
DR EMBL; U95515; AAB58275.1; -.
DR EMBL; U95516; AAB58276.1; -.
DR EMBL; U95517; AAB58277.1; -.
DR EMBL; U95518; AAB58278.1; -.
DR EMBL; U95519; AAB58279.1; -.
DR EMBL; U95520; AAB58280.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1978 MW; E716F226CC5BEB15 CRC64;

Query Match 28.6%; Score 28; DB 13; Length 18;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PDVEKPD 10
 |: | | | |
Db 11 PNGEKPD 17

RESULT 7

Q9PRY8

ID Q9PRY8 PRELIMINARY; PRT; 10 AA.
AC Q9PRY8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE Angiotensin I.
 OS Triakis scyllium (Leopard shark) (Triakis scyllia).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
 OC Triakis.
 OX NCBI_TaxID=30494;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94141412; PubMed=8308464;
 RA Takei Y., Hasegawa Y., Watanabe T.X., Nakajima K., Hazon N.;
 RT "A novel angiotensin I isolated from an elasmobranch fish."
 RL J. Endocrinol. 139:281-285(1993).
 SQ SEQUENCE 10 AA; 1284 MW; 20F02FD761E04B47 CRC64;

Query Match 27.6%; Score 27; DB 13; Length 10;
 Best Local Similarity 44.4%; Pred. No. 1e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 KPDLQPFQV 16
 :| : |||:
 Db 2 RPYIHPFQL 10

RESULT 8
 P82325

ID P82325 PRELIMINARY; PRT; 12 AA.
 AC P82325;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Unknown protein from 2D-page of thylakoid (SPOT106) (Fragment).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
 RX MEDLINE=20181728; PubMed=10715320;
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
 RA Adamska I., van Wijk K.J.;
 RT "Proteomics of the chloroplast: systematic identification and
 RT targeting analysis of lumenal and peripheral thylakoid proteins."
 RL Plant Cell 12:319-341(2000).
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
 CC PERIPHERY.
 CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.3, ITS MW IS: 18.2 KDA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0009579; C:thylakoid; IEA.
 KW Chloroplast; Thylakoid.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1236 MW; CEAC7ADC02633452 CRC64;

Query Match 27.6%; Score 27; DB 10; Length 12;

Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13
| ||:| |
Db 5 VNKPELLP 12

RESULT 9

Q9UCI2

ID Q9UCI2 PRELIMINARY; PRT; 16 AA.
AC Q9UCI2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tropomyosin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93195352; PubMed=8450225;
RA Das K.M., Dasgupta A., Mandal A., Geng X.;
RT "Autoimmunity to cytoskeletal protein tropomyosin. A clue to the
RT pathogenetic mechanism for ulcerative colitis."
RL J. Immunol. 150:2487-2493(1993).
SQ SEQUENCE 16 AA; 1960 MW; 7A26C4941E0A335E CRC64;

Query Match 27.6%; Score 27; DB 4; Length 16;
Best Local Similarity 38.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 5 DVEKPDLPQPFQVQ 17
| || ::| |::
Db 4 DEEKMEIQEIQLK 16

RESULT 10

Q8MNX0

ID Q8MNX0 PRELIMINARY; PRT; 18 AA.
AC Q8MNX0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Eystathioy T., Swevers L., Iatrou K.;
RT "The orphan nuclear receptors BmE75A, C and D from the silkworm Bombyx
RT mori: hormonal control and ovarian expression.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF332552; AAM43817.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2012 MW; 072C6D18DFF0ED5E CRC64;

Query Match 27.6%; Score 27; DB 5; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPDVEKP 9
: || | : |
Db 4 KPPSFEEP 11

RESULT 11

Q9S8G8

ID Q9S8G8 PRELIMINARY; PRT; 18 AA.
AC Q9S8G8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Proline-rich protein (Fragment).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=95277008; PubMed=7757337;
RA Esaka M., Hayakawa H.;
RT "Specific secretion of proline-rich proteins by salt-adapted winged
RT bean cells.";
RL Plant Cell Physiol. 36:441-446(1995).
SQ SEQUENCE 18 AA; 2252 MW; 4FD7D1DA18B5D94A CRC64;

Query Match 27.6%; Score 27; DB 10; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PDVEKP 9
| ||||
Db 9 PKVEKP 14

RESULT 12

Q9UEE2

ID Q9UEE2 PRELIMINARY; PRT; 13 AA.
AC Q9UEE2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ERGB transcription factor (Fragment).
GN FLI1.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Obata K., Hiraga H., Nojima T., Yoshida M.C., Abe S.;
 RT "Molecular analysis on the breakpoint region of a t(11:22)
 RT translocation in Ewing's sarcoma."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB012625; BAA32806.1; -.
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1541 MW; 2C677798CB566AB7 CRC64;

Query Match 26.5%; Score 26; DB 4; Length 13;
 Best Local Similarity 30.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 7 EKPDLPFQV 16
 ::| |::
 Db 2 QRPQDPFYQI 11

RESULT 13

Q9UWH3

ID Q9UWH3 PRELIMINARY; PRT; 15 AA.
 AC Q9UWH3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Keto-valine-ferredoxin oxidoreductase beta-subunit, VOR beta
 DE (Fragment).
 OS Thermococcus litoralis.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Thermococcus.
 OX NCBI_TaxID=2265;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96146528; PubMed=8550513;
 RA Heider J., Mai X., Adams M.W.;
 RT "Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a
 RT new and reversible coenzyme A-dependent enzyme involved in peptide
 RT fermentation by hyperthermophilic archaea."
 RL J. Bacteriol. 178:780-787(1996).
 SQ SEQUENCE 15 AA; 1740 MW; 5C0D6371E91D4C4F CRC64;

Query Match 26.5%; Score 26; DB 1; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.2e+03;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPF 14
 | ||:| ||
 Db 4 PADVKKRLTLPF 15

RESULT 14

Q9TR14

ID Q9TR14 PRELIMINARY; PRT; 15 AA.
AC Q9TR14;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Troponin-T homolog/proteolysis CONDITIONING INDICATOR peptide
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96187584; PubMed=8611748;
RA Nakai Y., Nishimura T., Shimizu M., Arai S.;
RT "Effects of freezing on the proteolysis of beef during storage at 4
RT degrees C.";
RL Biosci. Biotechnol. Biochem. 59:2255-2258(1995).
SQ SEQUENCE 15 AA; 1597 MW; C98A5B44A79E4777 CRC64;

Query Match 26.5%; Score 26; DB 6; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKPDL 11
|| | |::
Db 3 PPPAEVPEV 11

RESULT 15

Q9JK08

ID Q9JK08 PRELIMINARY; PRT; 17 AA.
AC Q9JK08;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
GN FBP2 OR FBPASE 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=20237676; PubMed=10773464;
RA Tillmann H., Stein S., Liehr T., Eschrich K.;
RT "Structure and chromosomal localization of the human and mouse muscle
RT fructose-1,6-bisphosphatase genes.";
RL Gene 247:241-253(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Stein S.;
RT "Mouse liver fructose-1,6-Bisphosphatase: Gene structure,

RT transcriptional start point, chromosomal localization, cDNA cloning,
RT characterization of the recombinant protein, and analysis of tissue-
RT specific expression.";
RL Arch. Biochem. Biophys. 0:0-0(0).
DR EMBL; AJ243021; CAB90668.1; -.
DR MGD; MGI:95491; Fbp2.
DR GO; GO:0042132; F:fructose-bisphosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
KW Hydrolase.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1887 MW; E2609FFD33922C8B CRC64;

Query Match 26.5%; Score 26; DB 11; Length 17;
Best Local Similarity 53.8%; Pred. No. 2.6e+03;
Matches 7; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 1 DQPPDVEKPDLP 13
|:| || |||
Db 4 DEPS--EKDALQP 14

RESULT 16

P90402

ID P90402 PRELIMINARY; PRT; 17 AA.
AC P90402;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vpr protein.
GN VPR.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z321B;
RX MEDLINE=97225063; PubMed=9071436;
RA Choi D.J., Dube S., Spicer T.P., Slade H.B., Jensen F.C., Poiesz B.J.;
RT "HIV type 1 isolate Z321, the strain used to make a therapeutic HIV
RT type 1 immunogen, is intersubtype recombinant.";
RL AIDS Res. Hum. Retroviruses 13:357-361(1997).
DR EMBL; U76035; AAB54106.1; -.
SQ SEQUENCE 17 AA; 1969 MW; 58CA75563F4457C7 CRC64;

Query Match 26.5%; Score 26; DB 15; Length 17;
Best Local Similarity 30.8%; Pred. No. 2.6e+03;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLP 13
:| |: : | :|
Db 2 EQAPEDQGPQREP 14

RESULT 17

Q9Q709

ID Q9Q709 PRELIMINARY; PRT; 17 AA.

AC Q9Q709;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Truncated Vpr.
 GN VPR.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VI997;
 RX MEDLINE=20436917; PubMed=10983640;
 RA Janssens W., Laukkanen T., Salminen M.O., Carr J.K.,
 RA Van der Auwera G., Heyndrickx L., van der Groen G., McCutchan F.E.;
 RT "HIV-1 subtype H near-full length genome reference strains and
 RT analysis of subtype-H-containing inter-subtype recombinants.";
 RL AIDS 14:1533-1543(2000).
 DR EMBL; AF190128; AAF18410.1; -.
 DR InterPro; IPR000012; RetroV_VpR/X.
 DR Pfam; PF00522; VPR; 1.
 KW AIDS.
 SQ SEQUENCE 17 AA; 1992 MW; 58CA70F63F4457C7 CRC64;

Query Match 26.5%; Score 26; DB 15; Length 17;
 Best Local Similarity 30.8%; Pred. No. 2.6e+03;
 Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLP 13
 :| |: :| :|
 Db 2 EQAPEDQGPQREP 14

RESULT 18

Q9X3E9

ID Q9X3E9 PRELIMINARY; PRT; 18 AA.
 AC Q9X3E9;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE Cytochrome b6/f complex subunit IV (Fragment).
 GN PETD.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 RT sorted from the Sargasso Sea and Gulf Stream.";
 RL Limnol. Oceanog. 43:1615-1630(1998).
 DR EMBL; AF070147; AAD20766.1; -.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2029 MW; EBF8A4E54FDCDE56 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 18;

Best Local Similarity 41.7%; Pred. No. 2.7e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 PDVEKPDLPFQ 15
||: ||: |
Db 7 PDLSDPKLRATQ 18

RESULT 19

Q9TWL5

ID Q9TWL5 PRELIMINARY; PRT; 18 AA.
AC Q9TWL5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 24 kDa chymotrypsin-like enzyme (Fragment).
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
RP SEQUENCE.
RX MEDLINE=95219141; PubMed=7704304;
RA Casu R.E., Pearson R.D., Jarmey J.M., Cadogan L.C., Riding G.A.,
RA Tellam R.L.;
RT "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,
RT enzymatic specificity and amino acid sequence deduced from mRNA."
RL Insect Mol. Biol. 3:201-211(1994).
DR InterPro; IPR009003; Cys_Ser_trypsin.
SQ SEQUENCE 18 AA; 2002 MW; AC29200B9B184300 CRC64;

Query Match 26.5%; Score 26; DB 5; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.7e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16
| | | : | |
Db 9 PGLFPYQV 16

RESULT 20

P83061

ID P83061 PRELIMINARY; PRT; 17 AA.
AC P83061;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative FK506-binding protein (FKBP) (Peptidyl-prolyl cis-trans
DE isomerase) (PPIase) (EC 5.2.1.8) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.

RA Schubert M., Peterson U., Funk C., Haas B., Schroeder W.P.,
 RA Kieselbach T.;
 RL Submitted (JUL-2001) to Swiss-Prot.
 CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
 CC SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 CC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
 CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0042027; F:cyclophilin-type peptidyl-prolyl cis-trans . . .; IEA.
 DR GO; GO:0004600; F:cyclophilin; IEA.
 DR GO; GO:0030051; F:FK506-sensitive peptidyl-prolyl cis-trans i. . .; IEA.
 DR GO; GO:0016853; F:isomerase activity; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR InterPro; IPR001179; FKBP_PPIase.
 KW Isomerase; Rotamase; Chloroplast.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1771 MW; E2013F998EFBF908 CRC64;

 Query Match 26.0%; Score 25.5; DB 10; Length 17;
 Best Local Similarity 66.7%; Pred. No. 3.1e+03;
 Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

 Qy 3 PPDVEKPD L 11
 ||: ||| |
 Db 4 PPE-EKPKL 11

RESULT 21

Q9UCT9
 ID Q9UCT9 PRELIMINARY; PRT; 18 AA.
 AC Q9UCT9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE PRG=PROLINE-rich glycoprotein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91373355; PubMed=1894623;
 RA Gillece-Castro B.L., Prakobphol A., Burlingame A.L., Leffler H.,
 RA Fisher S.J.;
 RT "Structure and bacterial receptor activity of a human salivary
 RT proline-rich glycoprotein.";
 RL J. Biol. Chem. 266:17358-17368(1991).
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0008368; F:Gram-negative bacterial binding; NAS.
 DR GO; GO:0009618; P:response to pathogenic bacteria; NAS.
 FT NON_TER 1 1
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1780 MW; 961F6FB0A83D2E40 CRC64;

Query Match 25.5%; Score 25; DB 4; Length 18;

Best Local Similarity 46.2%; Pred. No. 3.9e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLPFQ 15
|| ||: ||
Db 5 PPRPGKPEGPPPQ 17

RESULT 22

Q9S618

ID Q9S618 PRELIMINARY; PRT; 11 AA.
AC Q9S618;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream."
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070132; AAD20740.1; -.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 24.5%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 3.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKPD 11
::||||
Db 4 LKKPD 9

RESULT 23

P82328

ID P82328 PRELIMINARY; PRT; 12 AA.
AC P82328;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT110) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;

RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
 RA Adamska I., van Wijk K.J.;
 RT "Proteomics of the chloroplast: systematic identification and
 RT targeting analysis of lumenal and peripheral thylakoid proteins.";
 RL Plant Cell 12:319-341(2000).
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
 CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.0, ITS MW IS: 21.3 KDA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0009579; C:thylakoid; IEA.
 KW Chloroplast; Thylakoid.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1264 MW; 96691CBC663B1B01 CRC64;

Query Match 24.5%; Score 24; DB 10; Length 12;
 Best Local Similarity 62.5%; Pred. No. 3.6e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 PDVEKPD 11
 | ||| |
 Db 4 PTEEKPP 11

RESULT 24

Q9R3R6

ID Q9R3R6 PRELIMINARY; PRT; 13 AA.
 AC Q9R3R6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Cytochrome B6/F complex subunit IV (Fragment).
 GN PETD.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 RT sorted from the Sargasso Sea and Gulf Stream.";
 RL Limnol. Oceanog. 43:1615-1630(1998).
 DR EMBL; AF070222; AAD23275.1; -.
 DR EMBL; AF070221; AAD23273.1; -.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1522 MW; 4CDE4CC38013B763 CRC64;

Query Match 24.5%; Score 24; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 3.9e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKPD 11
 ::||| |
 Db 4 LKKPD 9

RESULT 25

Q9LB06

ID Q9LB06 PRELIMINARY; PRT; 17 AA.
 AC Q9LB06;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Cytochrome b6/f complex subunit IV (Fragment).
 GN PETD.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 RT sorted from the Sargasso Sea and Gulf Stream."
 RL Limnol. Oceanog. 43:1615-1630(1998).
 DR EMBL; AF070156; AAD23199.2; -.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1904 MW; CCEB69C5A202E54F CRC64;

Query Match 24.5%; Score 24; DB 2; Length 17;
 Best Local Similarity 44.4%; Pred. No. 5.2e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 PDVEKPDLO 12
 ||: | |:
 Db 3 PDLSDPKLR 11

RESULT 26

O67971

ID O67971 PRELIMINARY; PRT; 18 AA.
 AC O67971;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE B6/f complex subunit IV (Fragment).
 GN PETD.
 OS Synechococcus sp. (strain WH8103).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=29410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WH8103;
 RX MEDLINE=98123172; PubMed=9452521;
 RA Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;
 RT "Rapid diversification of marine picophytoplankton with dissimilar
 RT light-harvesting structures inferred from sequences of Prochlorococcus
 RT and Synechococcus (Cyanobacteria).";
 RL J. Mol. Evol. 46:188-201(1998).
 DR EMBL; AF001492; AAC05631.1; -.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2098 MW; C205CA0BB21CDE4C CRC64;

Query Match 24.5%; Score 24; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 5.6e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VEKPD L 11
::||||
Db 4 LKKPD L 9

RESULT 27

Q9UCS8

ID Q9UCS8 PRELIMINARY; PRT; 9 AA.
AC Q9UCS8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92075698; PubMed=1742316;
RA Ehnholm C., Bozas S.E., Tenkanen H., Kirszbaum L., Metso J.,
RA Murphy B., Walker I.D.;
RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40
RT protein of human blood are different proteins which both bind to
RT apolipoprotein A-I."
RL Biochim. Biophys. Acta 1086:255-260(1991).
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005319; F:lipid transporter activity; NAS.
DR GO; GO:0008203; P:cholesterol metabolism; ISS.
DR GO; GO:0006869; P:lipid transport; ISS.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 981 MW; 7FE37775A6C7776B CRC64;

Query Match 24.0%; Score 23.5; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 DQPPDVEKPD 10
|:| | |
Db 1 DEPPQ-SPPD 9

RESULT 28

Q9R735

ID Q9R735 PRELIMINARY; PRT; 9 AA.
AC Q9R735;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FkBA protein (Fragment).
GN FKBA.

OS Streptomyces chrysomallus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1899;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94341259; PubMed=8062824;
 RA Pahl A., Keller U.;
 RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
 RT of two FK506-binding domains with its gene transcriptionally coupled
 RT to the FKBP-12 gene.";
 RL EMBO J. 13:3472-3480(1994).
 DR EMBL; Z34523; CAA84282.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1047 MW; 9A8BCB07633B1045 CRC64;

Query Match 23.5%; Score 23; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 VEKPD L 11
 :|||::
 Db 3 IEKPEV 8

RESULT 29

P81715

ID P81715 PRELIMINARY; PRT; 14 AA.
 AC P81715;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Leupeptin-inactivating enzyme (EC 3.4.24.-) (LIE) (Fragment).
 OS Streptomyces exfoliatus (Streptomyces hydrogenans).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1905;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=SMF13;
 RX PubMed=9531495;
 RA Kim I.S., Kim Y.B., Lee K.J.;
 RT "Characterization of the leupeptin-inactivating enzyme from
 RT Streptomyces exfoliatus SMF13 which produces leupeptin.";
 RL Biochem. J. 331:539-545(1998).
 CC -!- FUNCTION: A LEUCINE-SPECIFIC METALLOPROTEASE THAT PLAYS A ROLE IN
 CC CONTROLLING THE AMOUNT OF LEUPEPTIN DURING COLONY DEVELOPMENT.
 CC OPTIMUM PH IS 9.0 AND TEMPERATURE IS 40 DEGREES CELSIUS.
 CC -!- FUNCTION: DEGRADATES LEUPEPTIN INTO THREE COMPONENTS, ACETYL-
 CC LEUCINE, LEUCINE AND ARGININAL.
 CC -!- CATALYTIC ACTIVITY: HAS A STRICT PREFERENCE FOR LEUCINE AT THE P1
 CC SITE.
 CC -!- ENZYME REGULATION: ACTIVITY IS INHIBITED BY METALLOPROTEASE
 CC INHIBITORS AND ACTIVATED BY MG2+ AND CA2+.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0008237; F:metallopeptidase activity; IEA.
KW Hydrolase; Metalloprotease..
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1373 MW; 14D627940C973260 CRC64;

Query Match 23.5%; Score 23; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPDV 6
|||:
Db 4 PPDI 7

RESULT 30

P97135

ID P97135 PRELIMINARY; PRT; 17 AA.
AC P97135;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GyrA protein (Fragment).
GN GYRA.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Ra;
RX MEDLINE=95072534; PubMed=7981652;
RA Madhusudan K., Ramesh V., Nagaraja V.;
RT "Molecular cloning of gyrA and gyrB genes of Mycobacterium
tuberculosis:analysis of nucleotide sequence.";
RL Biochem. Mol. Biol. Int. 33:651-660(1994).
DR EMBL; X78888; CAA55487.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1916 MW; EF0B750A36E365AE CRC64;

Query Match 23.5%; Score 23; DB 2; Length 17;
Best Local Similarity 36.4%; Pred. No. 7.5e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 PPDVEKPDLP 13
||| ::|
Db 7 PPDSLDRIEP 17

RESULT 31

Q7YMC5

ID Q7YMC5 PRELIMINARY; PRT; 18 AA.
AC Q7YMC5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PsbT (Fragment).
GN PSBT.

OS Pogonatum subulatum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Polytrichopsida; Polytrichales; Polytrichaceae; Pogonatum.
 OX NCBI_TaxID=172817;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Quandt D.;
 RT "The systematic position of Pulchrinodus inflatus (Pulchrinodaceae,
 RT Bryopsida) based on molecular data."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY122276; AAM88440.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 SQ SEQUENCE 18 AA; 2184 MW; 24635A05ED23942E CRC64;

Query Match 23.5%; Score 23; DB 8; Length 18;
 Best Local Similarity 50.0%; Pred. No. 7.9e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPDVE 7
 :||:|
 Db 8 EPPKIE 13

RESULT 32

Q9L5W6

ID Q9L5W6 PRELIMINARY; PRT; 10 AA.
 AC Q9L5W6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE RplA (Fragment).
 GN RPLA.
 OS Liberibacter africanus (subsp. capensis).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Candidatus Liberibacter.
 OX NCBI_TaxID=119494;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Garnier M., Jagoueix-Eveillard S., Cronje P., Le Roux H., Bove J.;
 RT "Genomic characterization of a Liberibacter present in an ornamental
 RT rutaceous tree, Calodendrum capense, in the western Cape province of
 RT South Africa. Proposal of 'candidatus Liberibacter africanus
 RT subspecies capensis'.";
 RL Int. J. Syst. Evol. Microbiol. 0:0-0(2000).
 DR EMBL; AF248498; AAF68451.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 1094 MW; C42894D5A5B72AB2 CRC64;

Query Match 22.4%; Score 22; DB 2; Length 10;
 Best Local Similarity 55.6%; Pred. No. 6.1e+03;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 KPDLQPFQV 16
 | || | |
 Db 2 KVDLSSFSV 10

RESULT 33

Q8HYM4

ID Q8HYM4 PRELIMINARY; PRT; 11 AA.
 AC Q8HYM4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Coagulation factor IX (Fragment).
 GN F9.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Susott E.E., Rollo W.A., Venta P.J., Ewart S.L.;
 RT "Characterization of 8 Feline Type I Markers."
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF459805; AAO15586.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1169 MW; 9C8E7EFC A05B02CA CRC64;

Query Match 22.4%; Score 22; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PDVE 7
 ||||
 Db 3 PDVE 6

RESULT 34

Q9RIU3

ID Q9RIU3 PRELIMINARY; PRT; 14 AA.
 AC Q9RIU3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE R-ras GTPase activating protein (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Iwashita S.;
 RT "5'-flanking region of R-ras GTPase activating protein."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB021982; BAA81903.1; -.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1594 MW; 3C91E28A0C8E3E28 CRC64;

Query Match 22.4%; Score 22; DB 11; Length 14;

Best Local Similarity 50.0%; Pred. No. 8.7e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 VEKPDLPFQ 15
||: |: ||
Db 3 VEEGLRVFQ 12

RESULT 35

O69142

ID O69142 PRELIMINARY; PRT; 15 AA.
AC O69142;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Protein SIC (Fragment).
GN SIC.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP1;
RX MEDLINE=98298075; PubMed=9632622;
RA Berge A., Rasmussen M., Bjorck L.;
RT "Identification of an insertion sequence located in a region encoding
RT virulence factors of Streptococcus pyogenes."
RL Infect. Immun. 66:3449-3453(1998).
DR EMBL; AF064540; AAC38769.1; -.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1552 MW; 87655FEF847401FF CRC64;

Query Match 22.4%; Score 22; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 9.4e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KPDLQPF 14
|| : |:
Db 4 KPSVTPY 10

RESULT 36

Q08936

ID Q08936 PRELIMINARY; PRT; 15 AA.
AC Q08936;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chloroplast 29 kDa ribonucleoprotein A (CP29A) (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.

RC TISSUE=LEAF;
 RA Ye L., Li Y., Fukami-Kobayashi F., Go M., Konishi T., Watanbe A.,
 RA Sugiura M.;
 RL Nucleic Acids Res. 19:6485-6490(1994).
 CC -!- FUNCTION: COULD BE INVOLVED IN SPLICING AND/OR PROCESSING OF
 CC CHLOROPLAST RNA'S.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
 KW Ribonucleoprotein; Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1682 MW; C97821104B9756C8 CRC64;

Query Match 22.4%; Score 22; DB 10; Length 15;
 Best Local Similarity 71.4%; Pred. No. 9.4e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DQPPDVE 7
 || |||
 Db 7 DQIEDVE 13

RESULT 37

Q9QVL2

ID Q9QVL2 PRELIMINARY; PRT; 16 AA.
 AC Q9QVL2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE MEPRIN=METALLOENDOPEPTIDASE (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91363409; PubMed=1888759;
 RA Flannery A.V., Macadam G.C., Beynon R.J.;
 RT "Immunological characterisation of different meprin species in mice."
 RL Biochim. Biophys. Acta 1079:119-122(1991).
 FT NON_TER 1 1
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1922 MW; B0379F6803B42FAD CRC64;

Query Match 22.4%; Score 22; DB 11; Length 16;
 Best Local Similarity 33.3%; Pred. No. 1e+04;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 10 DLQPFQVQS 18
 | :|:: :|
 Db 2 DFKPYEGES 10

RESULT 38

Q9EUP4

ID Q9EUP4 PRELIMINARY; PRT; 17 AA.

AC Q9EUP4;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cell division associated protein (Fragment).
 GN DIVIVA.
 OS Thermus thermophilus.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KT8;
 RA Spada S., Gibert Y., Pembroke J.T., Wall J.G.;
 RT "Cloning and characterisation of the ylmE homologue of Thermus
 RT thermophilus.";
 RL DNA Seq. 11:5007-5014(2001).
 DR EMBL; AJ297409; CAC21427.1; -.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 2084 MW; 0C642E1D509D87E3 CRC64;

Query Match 22.4%; Score 22; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 DLQPFQVQ 17
 || | | :
 Db 2 DLSPLDVR 9

RESULT 39

O46667

ID O46667 PRELIMINARY; PRT; 17 AA.
 AC O46667;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Glucose-6-phosphate dehydrogenase (Fragment).
 GN G6PD.
 OS Macropus robustus robustus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=35580;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224585; PubMed=9060417;
 RA Loebel D.A., Johnston P.G.;
 RT "Analysis of the intron-exon structure of the G6PD gene of the
 RT wallaroo (Macropus robustus) by polymerase chain reaction.";
 RL Mamm. Genome 8:146-147(1997).
 DR EMBL; U53779; AAC48792.2; -.
 DR EMBL; U53778; AAC48792.2; JOINED.
 DR GO; GO:0004345; F:glucose-6-phosphate 1-dehydrogenase activity; IEA.
 DR GO; GO:0006006; P:glucose metabolism; IEA.
 DR InterPro; IPR001282; G6PD.
 DR Pfam; PF02781; G6PD_C; 1.
 FT NON_TER 1 1

FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2039 MW; 3A5B76F61F908B21 CRC64;

Query Match 22.4%; Score 22; DB 6; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DVEKPD 10
||: ||
Db 12 DVKLPD 17

RESULT 40

Q95M99

ID Q95M99 PRELIMINARY; PRT; 17 AA.
AC Q95M99;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypoxanthine guanine phosphoribosyltransferase 1 (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21314992; PubMed=11421942;
RA Shubitowski D.M., Venta P.J., Douglass C.L., Zhou R.-X., Ewart S.L.;
RT "Polymorphism identification within 50 equine gene-specific sequence
RT tagged sites.";
RL Anim. Genet. 32:78-78(2001).
DR EMBL; AY008794; AAG40103.1; -.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
KW Glycosyltransferase; Transferase.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1973 MW; 893D20A6378F3311 CRC64;

Query Match 22.4%; Score 22; DB 6; Length 17;
Best Local Similarity 33.3%; Pred. No. 1.1e+04;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 8 KPDLQPFQV 16
:|| |::
Db 5 RPDFVGFEI 13

RESULT 41

Q9QVC6

ID Q9QVC6 PRELIMINARY; PRT; 17 AA.
AC Q9QVC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE DW85 protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92291078; PubMed=1601872;
 RA Subramaniam V.N., bin Mohd Yusoff A.R., Wong S.H., Lim G.B., Chew M.,
 RA Hong W.;
 RT "Biochemical fractionation and characterization of proteins from
 RT Golgi-enriched membranes.";
 RL J. Biol. Chem. 267:12016-12021(1992).
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1949 MW; BC939B267EF49CB7 CRC64;

Query Match 22.4%; Score 22; DB 11; Length 17;
 Best Local Similarity 40.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPD 10
 | | | : |
 Db 3 DYPEDXSQSD 12

RESULT 42

Q9QVC2

ID Q9QVC2 PRELIMINARY; PRT; 17 AA.
 AC Q9QVC2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Kallikrein light chain N-terminus (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92329502; PubMed=1320938;
 RA Wang C., Tang C.Q., Zhou G.X., Chao L., Chao J.;
 RT "Biochemical characterization and substrate specificity of rat
 RT prostate kallikrein (S3): comparison with tissue kallikrein, tonin and
 RT T-kininogenase.";
 RL Biochim. Biophys. Acta 1121:309-316(1992).
 DR HSSP; P36368; 1A05.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1852 MW; A403B510DF5C096D CRC64;

Query Match 22.4%; Score 22; DB 11; Length 17;
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QPFQV 16
 ||:||
 Db 12 QPWQV 16

RESULT 43

Q919B0

ID Q919B0 PRELIMINARY; PRT; 17 AA.
 AC Q919B0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE E7 protein (Fragment).
 GN E7.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16E6CC14;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF404705; AAL01367.1; -.
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 1998 MW; 4471DB6BF776889B CRC64;

Query Match 22.4%; Score 22; DB 12; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
 ||||
 Db 14 DLQP 17

RESULT 44

Q56610

ID Q56610 PRELIMINARY; PRT; 18 AA.
 AC Q56610;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE AccA (Fragment).
 GN ACCA.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C6706;
 RX MEDLINE=97074686; PubMed=8917113;
 RA Franco A., Peir-En Y., Johnson J., Barry E.M., Guerra H., Maurer R.,
 RA Morris J.G.;
 RT "Cloning and characterization of dnaE, encoding the catalytic subunit
 RT of replicative DNA polymerase III, from Vibrio cholerae strain
 RT C6706."
 RL Gene 175:281-283(1996).
 DR EMBL; U30472; AAC44579.1; -.

FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2153 MW; 18EBCDAD212842EF CRC64;

Query Match 22.4%; Score 22; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DVEKP 9
| |||
Db 7 DFEKP 11

RESULT 45

Q9POM3

ID Q9POM3 PRELIMINARY; PRT; 18 AA.
AC Q9POM3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Polymyositis/scleroderma autoantigen 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bliskovsky V., Miller M., Mock B.;
RT "Structure and localization of mouse PM-Scl genes."
RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF152839; AAF73199.1; -.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2025 MW; A1F292BC77872D67 CRC64;

Query Match 22.4%; Score 22; DB 4; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.1e+04;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PPDVEKP 9
|| :|
Db 3 PPSTREP 9

RESULT 46

Q96C65

ID Q96C65 PRELIMINARY; PRT; 18 AA.
AC Q96C65;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;

RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC014643; AAH14643.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 18 AA; 2105 MW; 3874A0D25D91AC9C CRC64;

Query Match 22.4%; Score 22; DB 4; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.1e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 7 EKPDLPFQ 15
| |:
Db 7 ELESRLPFE 15

RESULT 47

Q9WTP8

ID Q9WTP8 PRELIMINARY; PRT; 18 AA.
AC Q9WTP8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE R-ras GTPase activating protein (Fragment).
GN R-RAS GAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Iwashita S., Kobayashi M.;
RT "NGF-mediated downregulation of R-ras GAP expression.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB020479; BAA78368.1; -.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2104 MW; 6BC3355FDC91E28A CRC64;

Query Match 22.4%; Score 22; DB 11; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 VEKPDLPFQ 15
| |:
Db 3 VEEGLRVFQ 12

RESULT 48

Q919D5

ID Q919D5 PRELIMINARY; PRT; 18 AA.
AC Q919D5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.

OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16E6CC1;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF404692; AAL01341.1; -.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.4%; Score 22; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
 ||||
 Db 14 DLQP 17

RESULT 49

Q919B3

ID Q919B3 PRELIMINARY; PRT; 18 AA.
 AC Q919B3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE E7 protein (Fragment).
 GN E7.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16E6CC12;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF404703; AAL01364.1; -.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.4%; Score 22; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
 ||||
 Db 14 DLQP 17

RESULT 50

Q919B5

ID Q919B5 PRELIMINARY; PRT; 18 AA.
 AC Q919B5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE E7 protein (Fragment).
 GN E7.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPV16E6CC11;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF404702; AAL01362.1; -.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.4%; Score 22; DB 12; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
 ||||
 Db 14 DLQP 17

Search completed: July 4, 2004, 04:45:29
 Job time : 33.6269 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:26 ; Search time 6.1791 Seconds
 (without alignments)
 151.683 Million cell updates/sec

Title: US-09-641-802-3
 Perfect score: 98
 Sequence: 1 DQPPDVEKPDLPFQVQS 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 952

Minimum DB seq length: 7
 Maximum DB seq length: 18

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	31	31.6	15	1 MK1_PALPR	P80408 palomena pr
2	31	31.6	15	1 MK2A_PALPR	P80409 palomena pr
3	31	31.6	16	1 MK2B_PALPR	P80410 palomena pr
4	31	31.6	16	1 MK3_PALPR	P80411 palomena pr
5	30	30.6	10	1 URE3_MORMO	P17339 morganella
6	23	23.5	9	1 COXE_THUOB	P80975 thunnus obe
7	22	22.4	12	1 PPK4_PERAM	P82619 periplaneta
8	22	22.4	12	1 TKN2_KASMA	P08614 kassina mac
9	22	22.4	16	1 IBP4_PIG	P24854 sus scrofa
10	21	21.4	7	1 UF04_MOUSE	P38642 mus musculu
11	21	21.4	12	1 TKN1_KASMA	P08613 kassina mac
12	21	21.4	15	1 VORA_METTM	P80907 methanobact
13	20	20.4	10	1 SLAP_BACTG	P49325 bacillus th
14	20	20.4	10	1 UPA2_HUMAN	P30088 homo sapien
15	20	20.4	11	1 MORN_HUMAN	P01163 homo sapien
16	20	20.4	12	1 XYLA_STRVN	P14405 streptomyce
17	20	20.4	13	1 ACT7_SOYBN	P15987 glycine max

18	20	20.4	13	1	BRK_PARID	P42717	parapolybia
19	20	20.4	13	1	ECDE_LYMDI	P80941	lymantria d
20	20	20.4	17	1	ACT6_SOYBN	P15986	glycine max
21	20	20.4	17	1	PSBL_SYNVU	P12241	synechococc
22	20	20.4	17	1	VESP_VESMC	P57672	vespula mac
23	20	20.4	18	1	FIBA_LAMGL	P14454	lama glama
24	19.5	19.9	11	1	BPP3_BOTIN	P30423	bothrops in
25	19.5	19.9	11	1	BPP4_BOTIN	P30424	bothrops in
26	19	19.4	8	1	AL12_CARMA	P81815	carcinus ma
27	19	19.4	9	1	KNL3_BOMVA	P83058	bombina var
28	19	19.4	10	1	FARP_LOCFI	P38553	locusta mig
29	19	19.4	11	1	BRK_MEGFL	P12797	megascolia
30	19	19.4	12	1	TKN_KASSE	P08611	kassina sen
31	19	19.4	13	1	ODPA_CANFA	P49823	canis famil
32	19	19.4	17	1	SRV_URSAR	P36396	ursus arcto
33	18.5	18.9	11	1	BPPB_AGKHA	P01021	agkistrodon
34	18	18.4	9	1	LMT3_LOCFI	P41489	locusta mig
35	18	18.4	10	1	FAR6_PANRE	P82660	panagrellus
36	18	18.4	12	1	FARI_CALVO	P41869	calliphora
37	18	18.4	12	1	HS9A_RAT	P82995	rattus norv
38	18	18.4	13	1	EP65_HUMAN	P54963	homo sapien
39	18	18.4	13	1	PEDI_HYDAT	P80578	hydra atten
40	18	18.4	13	1	TY13_PHYRO	P04096	phyllomedus
41	18	18.4	14	1	MARI_ALTSP	P29399	alteromonas
42	18	18.4	15	1	HS11_PINPS	P81083	pinus pinas
43	18	18.4	15	1	PSAO_CUCSA	P42052	cucumis sat
44	18	18.4	15	1	UC23_MAIZE	P80629	zea mays (m
45	18	18.4	16	1	LPK1_LOCFI	P20404	locusta mig
46	18	18.4	18	1	LCTN_LAMGL	P83315	lama glama
47	17	17.3	10	1	BPP2_BOTJA	P01022	bothrops ja
48	17	17.3	10	1	BPP8_BOTIN	P30426	bothrops in
49	17	17.3	11	1	EFG_CLOPA	P81350	clostridium
50	17	17.3	11	1	RRPL_CHAV	P13179	chandipura
51	17	17.3	11	1	TKNA_GADMO	P28498	gadus morhu
52	17	17.3	12	1	FIF1_SARBU	P83349	sarcophaga
53	17	17.3	12	1	PPK4_PERFU	P82690	periplaneta
54	17	17.3	13	1	BPP1_BOTJA	P01020	bothrops ja
55	17	17.3	13	1	EI21_LITRU	P82097	litoria rub
56	17	17.3	13	1	EI22_LITRU	P82098	litoria rub
57	17	17.3	13	1	SODM_CANFA	P54712	canis famil
58	17	17.3	13	1	YPE2_LACLC	P42021	lactococcus
59	17	17.3	14	1	SODN_STRGR	P80732	streptomyce
60	17	17.3	14	1	TAT_HV1Z8	P12511	human immun
61	17	17.3	15	1	AF1L_MALPA	P83141	malva parvi
62	17	17.3	15	1	PRP_MYCBO	P80149	mycobacteri
63	17	17.3	15	1	RS6_BACST	P59682	bacillus st
64	17	17.3	15	1	UBL1_MONDO	P50103	monodelphis
65	17	17.3	15	1	UP02_METAN	P83439	metarhizium
66	17	17.3	16	1	AF1S_MALPA	P83140	malva parvi
67	17	17.3	17	1	A45K_MYCBO	P80069	mycobacteri
68	17	17.3	17	1	APID_BOMPA	P81464	bombus pasc
69	17	17.3	17	1	EFG_THEAQ	Q01697	thermus aqu
70	17	17.3	18	1	SODM_MYCHA	P80582	mycobacteri
71	16.5	16.8	11	1	BPP_AGKHP	P04562	agkistrodon
72	16	16.3	7	1	LANC_CARUI	P36960	carnobacter
73	16	16.3	8	1	PPK3_PERAM	P82618	periplaneta
74	16	16.3	9	1	ULAH_HUMAN	P31934	homo sapien

75	16	16.3	10	1	GON1_ALLMI	P37041	alligator m
76	16	16.3	11	1	TKN1_UPERU	P08612	uperoleia r
77	16	16.3	11	1	TKNA_RANRI	P29207	rana ridibu
78	16	16.3	11	1	TKND_RANCA	P22691	rana catesb
79	16	16.3	13	1	ADFB_TENMO	P83109	tenebrio mo
80	16	16.3	13	1	BLAC_STRGR	P81173	streptomyce
81	16	16.3	14	1	ANGT_HORSE	P01016	equus cabal
82	16	16.3	14	1	TAT_HV1W2	P12509	human immun
83	16	16.3	15	1	COXJ_THUOB	P80979	thunnus obe
84	16	16.3	15	1	PDGB_PIG	P20034	sus scrofa
85	16	16.3	15	1	PH2_PERAM	P82695	periplaneta
86	16	16.3	15	1	SODM_STRGR	P80733	streptomyce
87	16	16.3	16	1	CXAB_CONPE	P50985	conus penna
88	16	16.3	16	1	FOR1_MYRGU	P81438	myrmecia gu
89	16	16.3	18	1	CPAX_BOVIN	P22779	bos taurus
90	16	16.3	18	1	FIBA_CAMDR	P14444	camelus dro
91	16	16.3	18	1	FIXA_RHILE	P14313	rhizobium l
92	16	16.3	18	1	HEMH_THETS	P80155	theromyzon
93	16	16.3	18	1	RL23_HALCU	P05975	halobacteri
94	16	16.3	18	1	TKN2_SCYCA	P08609	scyliorhinu
95	15	15.3	7	1	TPFY_PACDA	P83455	pachymedusa
96	15	15.3	8	1	ANG2_BOTJA	Q10582	bothrops ja
97	15	15.3	8	1	B44K_PORGI	P81886	porphyromon
98	15	15.3	8	1	UPA1_HUMAN	P30087	homo sapien
99	15	15.3	9	1	AL10_CARMA	P81813	carcinus ma
100	15	15.3	9	1	FRF1_SARBU	P83350	sarcophaga

ALIGNMENTS

RESULT 1

MK1_PALPR

ID MK1_PALPR STANDARD; PRT; 15 AA.

AC P80408;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Metalnukowin I.

OS Palomena prasina (Green shield bug).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;

OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;

OC Palomena.

OX NCBI_TaxID=55431;

RN [1]

RP SEQUENCE.

RC TISSUE=Hemolymph;

RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;

RT "The inducible antibacterial peptides of the hemipteran insect

RT Palomena prasina: identification of a unique family of proline-rich peptides and of a novel insect defensin.";

RL J. Insect Physiol. 42:81-89(1996).

CC -!- FUNCTION: Antibacterial peptide active against Gram-negative bacteria.

CC -!- INDUCTION: By bacterial infection.

KW Antibiotic; Insect immunity.

SQ SEQUENCE 15 AA; 1838 MW; 21407E663CE46299 CRC64;

Query Match 31.6%; Score 31; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 67;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VEKPDLP 13
|:|:|:|:|
Db 1 VDKPDYRP 8

RESULT 2

MK2A_PALPR

ID MK2A_PALPR STANDARD; PRT; 15 AA.

AC P80409;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Metalnikowin IIA.

OS Palomena prasina (Green shield bug).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;

OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;

OC Palomena.

OX NCBI_TaxID=55431;

RN [1]

RP SEQUENCE.

RC TISSUE=Hemolymph;

RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;

RT "The inducible antibacterial peptides of the hemipteran insect

RT Palomena prasina: identification of a unique family of proline-rich
peptides and of a novel insect defensin.";

RL J. Insect Physiol. 42:81-89(1996).

CC -!- FUNCTION: Antibacterial peptide active against Gram-negative
bacteria.

CC -!- INDUCTION: By bacterial infection.

KW Antibiotic; Insect immunity.

SQ SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;

Query Match 31.6%; Score 31; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 67;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VEKPDLP 13
|:|:|:|:|
Db 1 VDKPDYRP 8

RESULT 3

MK2B_PALPR

ID MK2B_PALPR STANDARD; PRT; 16 AA.

AC P80410;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Metalnikowin IIB.

OS Palomena prasina (Green shield bug).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
 OC Palomena.
 OX NCBI_TaxID=55431;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina: identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin."
 RL J. Insect Physiol. 42:81-89(1996).
 CC -!- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -!- INDUCTION: By bacterial infection.
 KW Antibiotic; Insect immunity.
 SQ SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;

 Query Match 31.6%; Score 31; DB 1; Length 16;
 Best Local Similarity 62.5%; Pred. No. 71;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 Qy 6 VEKPDLPQ 13
 |:| | | :|
 Db 1 VDKPDYRP 8

RESULT 4

MK3_PALPR

ID MK3_PALPR STANDARD; PRT; 16 AA.
 AC P80411;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Metalnikowin III.
 OS Palomena prasina (Green shield bug).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
 OC Palomena.
 OX NCBI_TaxID=55431;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina: identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin."
 RL J. Insect Physiol. 42:81-89(1996).
 CC -!- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -!- INDUCTION: By bacterial infection.
 KW Antibiotic; Insect immunity.
 SQ SEQUENCE 16 AA; 2024 MW; A9E3835D063B9462 CRC64;

Query Match 31.6%; Score 31; DB 1; Length 16;

Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VEKPDLPQ 13
|:|:|:|
Db 1 VDKPDYRP 8

RESULT 5

URE3_MORMO

ID URE3_MORMO STANDARD; PRT; 10 AA.
AC P17339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Urease gamma subunit (EC 3.5.1.5) (Urea amidohydrolase gamma subunit)
DE (Urease 6 kDa subunit) (Fragment).
GN UREA.
OS *Morganella morganii* (*Proteus morganii*).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Morganella*.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE.
RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences."
RL J. Bacteriol. 172:3073-3080(1990).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- SUBUNIT: (Alpha, beta, gamma)(3) (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the urease gamma subunit family.
DR PIR; C35389; C35389.
DR HAMAP; MF_00739; -, 1.
KW Hydrolase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 30.6%; Score 30; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPDVEK 8
|:|:|:|
Db 5 PPEVEK 10

RESULT 6

COXE_THUOB

ID COXE_THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide VIa (EC 1.9.3.1) (Fragment).
OS *Thunnus obesus* (Bigeye tuna).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OX NCBI_TaxID=8241;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=97454291; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver.";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
 CC chains of cytochrome c oxidase, the terminal oxidase in
 CC mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIa family.
 DR PIR; S77984; S77984.
 DR InterPro; IPR001349; COX6A.
 DR PROSITE; PS01329; COX6A; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 23.5%; Score 23; DB 1; Length 9;
 Best Local Similarity 37.5%; Pred. No. 1.4e+05;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 7 EKPDLQPF 14
 |:|: |:
 Db 2 EQPEFVPY 9

RESULT 7

PPK4_PERAM

ID PPK4_PERAM STANDARD; PRT; 12 AA.
 AC P82619;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-4 (Pea-PK-4) (YXPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and

RT abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
 CC -!- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 12 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1449 MW; FA7A3049FF42CAA1 CRC64;

Query Match 22.4%; Score 22; DB 1; Length 12;
 Best Local Similarity 55.6%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 PPDVEKPDL 11
 | || | |
 Db 4 PHDVYSPRL 12

RESULT 8

TKN2_KASMA

ID TKN2_KASMA STANDARD; PRT; 12 AA.
 AC P08614;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hylambatin.
 OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
 OC Kassina.
 OX NCBI_TaxID=8414;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
 RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
 RT hylambatin, in the skin of the African rhacophorid frog Hylambates
 RT maculatus.";
 RL Biomed. Res. 2:613-617(1981).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S07436; S07436.
 DR InterPro; IPR002040; Tachy_Neurokinin.

DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;

Query Match 22.4%; Score 22; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPDVEK 8
||| ::
Db 2 PPDPR 7

RESULT 9

IBP4_PIG

ID IBP4_PIG STANDARD; PRT; 16 AA.
AC P24854;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92109718; PubMed=1722398;
RA Coleman M.E., Pan Y.-C.E., Etherton T.D.;
RT "Identification and NH2-terminal amino acid sequence of three
RT insulin-like growth factor-binding proteins in porcine serum.";
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -!- FUNCTION: IGF-binding proteins prolong the half-life of the IGFs
CC and have been shown to either inhibit or stimulate the growth
CC promoting effects of the IGFs on cell culture. They alter the
CC interaction of IGFs with their cell surface receptors.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 IGFBP domain.
CC -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.
DR PIR; JH0517; JH0517.
DR InterPro; IPR000867; Insl_gro_fac_pr.
DR InterPro; IPR000716; Thyroglobulin_1.
DR PROSITE; PS00222; IGF_BINDING; PARTIAL.
DR PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 22.4%; Score 22; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPDVEK 8

Db || ||
8 PPSEEK 13

RESULT 10

UF04_MOUSE

ID UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.0, its MW is: 46 kDa.
FT NON TER 7 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 21.4%; Score 21; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPD 5
 :|||
Db 2 KPPD 5

RESULT 11

TKN1_KASMA

ID TKN1_KASMA STANDARD; PRT; 12 AA.
AC P08613;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hylambates kassinin ([Glu2,Pro5]kassinin).
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8414;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT hylambatin, in the skin of the African rhacophorid frog Hylambates

RT maculatus.";
 RL Biomed. Res. 2:613-617(1981).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S10059; S10059.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 12 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1376 MW; 3E756D279DD6DAB7 CRC64;

Query Match 21.4%; Score 21; DB 1; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 DVEKPD 10
 | |||
 Db 1 DEPKPD 6

RESULT 12

VORA_METTM

ID VORA_METTM STANDARD; PRT; 15 AA.
 AC P80907;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ketoisovalerate oxidoreductase subunit vorA (EC 1.-.-.) (VOR) (2-
 DE oxoisovalerate oxidoreductase alpha chain) (2-oxoisovalerate-
 DE ferredoxin oxidoreductase alpha subunit) (Fragment).
 GN VORA.
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=79929;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97261844; PubMed=9108258;
 RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
 RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
 RT in Methanobacterium thermoautotrophicum."
 RL Eur. J. Biochem. 244:862-868(1997).
 CC -!- SUBUNIT: HETEROTRIMER OF THE VORA, VORB AND VORC SUBUNITS.
 CC -!- MISCELLANEOUS: Has a pH optimum of 9.7 and an optimal temperature
 CC of 75 degrees Celsius.
 KW Oxidoreductase.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1779 MW; 31320B6531CA528F CRC64;

Query Match 21.4%; Score 21; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VEKPD 10
: |||
Db 5 IRKPD 9

RESULT 13

SLAP_BACTG

ID SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=90078111; PubMed=2592346;
RA Luckevich M.D., Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL J. Bacteriol. 171:6656-6667(1989).
CC -!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
CC of proteins which coat the surface of bacteria.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.
DR PIR; A60476; A60476.
KW Cell wall; S-layer.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;

Query Match 20.4%; Score 20; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PDLQP 13
||: |
Db 6 PDVXP 10

RESULT 14

UPA2_HUMAN

ID UPA2_HUMAN STANDARD; PRT; 10 AA.
AC P30088;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing."
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.4, its MW is: 49 kDa.
 DR SWISS-2DPAGE; P30088; HUMAN.
 FT NON_TER 1 1
 FT UNSURE 6 6
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;

Query Match 20.4%; Score 20; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPD 5
 |||
 Db 5 PPD 7

RESULT 15

MORN_HUMAN

ID MORN_HUMAN STANDARD; PRT; 11 AA.
 AC P01163;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Morphogenetic neuropeptide (Head activator) (HA).
 OS Homo sapiens (Human),
 OS Rattus norvegicus (Rat),
 OS Bos taurus (Bovine),
 OS Anthopleura elegantissima (Sea anemone), and
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Human, Rat, and Bovine;
 RX MEDLINE=82035850; PubMed=7290191;
 RA Bodenmuller H., Schaller H.C.;
 RT "Conserved amino acid sequence of a neuropeptide, the head activator,
 RT from coelenterates to humans."
 RL Nature 293:579-580(1981).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=A.elegantissima, and H.attenuata;
 RA Schaller H.C., Bodenmuller H.;
 RT "Isolation and amino acid sequence of a morphogenetic peptide from
 RT hydra."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).

RN [3]
 RP SYNTHESIS.
 RX MEDLINE=82050803; PubMed=7297679;
 RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
 RT "Synthesis of a new neuropeptide, the head activator from hydra.";
 RL FEBS Lett. 131:317-321(1981).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=90059923; PubMed=2583101;
 RA Schaller H.C., Druffel-Augustin S., Dubel S.;
 RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
 RT in the G2/mitosis transition.";
 RL EMBO J. 8:3311-3318(1989).
 CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells
 CC in the G2/mitosis transition.
 CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra
 CC and was called head activator by the authors, because it induced
 CC head-specific growth and differentiation in this animal. It has
 CC been found in mammalian intestine and hypothalamus.
 DR PIR; A01427; YHRT.
 DR PIR; A93900; YHXA.E.
 DR PIR; B01427; YHHU.
 DR PIR; B93900; YHJFHY.
 DR PIR; C01427; YHBO.
 DR GK; P01163; -.
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

 Query Match 20.4%; Score 20; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 2.3e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 Qy 2 QPPDVEK 8
 ||| |
 Db 1 QPPGGSK 7

RESULT 16

XYLA_STRVN
 ID XYLA_STRVN STANDARD; PRT; 12 AA.
 AC P14405;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Xylose isomerase (EC 5.3.1.5) (Fragment).
 GN XYLA.
 OS Streptomyces violaceoruber.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1935;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=LMG 7183;
 RX MEDLINE=90104230; PubMed=2604694;
 RA Vangrysperre W., Ampe C., Kersters-Hilderson H., Tempst P.;
 RT "Single active-site histidine in D-xylose isomerase from Streptomyces

RT violaceoruber. Identification by chemical derivatization and peptide
 RT mapping.";
 RL Biochem. J. 263:195-199(1989).
 CC -!- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
 CC -!- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the xylose isomerase family.
 DR HAMAP; MF_00455; -; 1.
 DR InterPro; IPR001998; Xylose_isom.
 DR PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
 DR PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
 KW Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.
 FT NON_TER 1 1
 FT ACT_SITE 5 5
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1375 MW; E749268EB1AAAAA1 CRC64;

Query Match 20.4%; Score 20; DB 1; Length 12;
 Best Local Similarity 80.0%; Pred. No. 2.5e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 DLQPF 14
 || ||
 Db 8 DLIPF 12

RESULT 17

ACT7_SOYBN

ID ACT7_SOYBN STANDARD; PRT; 13 AA.
 AC P15987;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Actin 7 (Fragment).
 GN SAC7.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Wayne;
 RX MEDLINE=91346640; PubMed=2102831;
 RA Pearson L., Meagher R.B.;
 RT "Diverse soybean actin transcripts contain a large intron in the 5'
 RT untranslated leader: structural similarity to vertebrate muscle actin
 RT genes.";
 RL Plant Mol. Biol. 14:513-526(1990).
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells.
 CC -!- FUNCTION: Essential component of cell cytoskeleton; plays an
 CC important role in cytoplasmic streaming, cell shape determination,
 CC cell division, organelle movement and extension growth.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- MISCELLANEOUS: There are at least 16 actin genes in soybean.
 CC -!- SIMILARITY: Belongs to the actin family.
 CC -----
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 CC -----
 DR EMBL; X17120; CAA34980.1; -.
 DR PIR; S15755; S15755.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR PROSITE; PS00406; ACTINS_1; PARTIAL.
 DR PROSITE; PS00432; ACTINS_2; PARTIAL.
 DR PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
 KW Structural protein; Multigene family.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;

Query Match 20.4%; Score 20; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
 |:||
 Db 6 DIQP 9

RESULT 18

BRK_PARID

ID BRK_PARID STANDARD; PRT; 13 AA.
 AC P42717;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Waspkinin.
 OS Parapolybia indica.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Polistinae; Parapolybia.
 OX NCBI_TaxID=31921;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Toki T., Yasuhara T., Nakajima T.;
 RT "Isolation and sequential analysis of peptides on the venom sac of
 RT Parapolybia indica."
 RL Eisei Dobutsu 39:105-111(1988).
 CC -!- FUNCTION: Induces smooth muscle contraction.
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -!- SIMILARITY: Belongs to the bradykinin family.
 KW Bradykinin; Vasodilator; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA; 1573 MW; 2673CB3D83ECC867 CRC64;

Query Match 20.4%; Score 20; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
| ||:
Db 6 PGFSPFR 12

RESULT 19

ECDE_LYMDI

ID ECDE_LYMDI STANDARD; PRT; 13 AA.
AC P80941;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Testis ecdysiotropin peptide E (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97387807; PubMed=9243792;
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae."
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -!- FUNCTION: Stimulates synthesis of ecdysteroid in the testes of
CC larvae and pupae.
SQ SEQUENCE 13 AA; 1357 MW; 1841B4CA3275B764 CRC64;

Query Match 20.4%; Score 20; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 2.7e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PDVEKPD 10
|: : ||
Db 5 PNPDTPD 11

RESULT 20

ACT6_SOYBN

ID ACT6_SOYBN STANDARD; PRT; 17 AA.
AC P15986;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 6 (Fragment).
GN SAC6.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Wayne;
 RX MEDLINE=91346640; PubMed=2102831;
 RA Pearson L., Meagher R.B.;
 RT "Diverse soybean actin transcripts contain a large intron in the 5'
 RT untranslated leader: structural similarity to vertebrate muscle actin
 RT genes.";
 RL Plant Mol. Biol. 14:513-526(1990).
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved
 CC in various types of cell motility and are ubiquitously expressed
 CC in all eukaryotic cells.
 CC -!- FUNCTION: Essential component of cell cytoskeleton; plays an
 CC important role in cytoplasmic streaming, cell shape determination,
 CC cell division, organelle movement and extension growth.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- MISCELLANEOUS: There are at least 16 actin genes in soybean.
 CC -!- SIMILARITY: Belongs to the actin family.
 CC -----
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 CC -----
 DR EMBL; X17119; CAA34979.1; -.
 DR PIR; S15754; S15754.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR PROSITE; PS00406; ACTINS_1; PARTIAL.
 DR PROSITE; PS00432; ACTINS_2; PARTIAL.
 DR PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
 KW Structural protein; Multigene family.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;

Query Match 20.4%; Score 20; DB 1; Length 17;
 Best Local Similarity 75.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DLQP 13
 |:||
 Db 6 DIQP 9

RESULT 21

PSBL_SYNVU

ID PSBL_SYNVU STANDARD; PRT; 17 AA.
 AC P12241;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Photosystem II reaction center L protein (PSII 5 kDa protein)

DE (Fragment).
GN PSBL.
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCBI_TaxID=32053;
RN [1]
RP SEQUENCE.
RA Ikeuchi M., Koike H., Inoue Y.;
RT "Identification of psbI and psbL gene products in cyanobacterial
RT photosystem II reaction center preparation.";
RL FEBS Lett. 251:155-160(1989).
CC -!- FUNCTION: Not known, it is however required for PSII activity.
CC -!- SUBCELLULAR LOCATION: Cellular thylakoid membrane.
CC -!- SIMILARITY: Belongs to the psbL family.
DR PIR; S05033; S05033.
DR HAMAP; MF_01317; -; 1.
DR InterPro; IPR003372; PSII_PsbL.
DR Pfam; PF02419; PsbL; 1.
KW Photosynthesis; Thylakoid; Photosystem II; Reaction center.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;

Query Match 20.4%; Score 20; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 3.6e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 9 PDLQPFQV 16
|: || ::
Db 5 PNRQPVEL 12

RESULT 22

VESP_VESMC

ID VESP_VESMC STANDARD; PRT; 17 AA.
AC P57672;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespulakinin 1 [Contains: Vespulakinin 2].
OS Vespa maculifrons (Eastern yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7453;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=76114777; PubMed=1247511;
RA Yoshida H., Geller R.G., Pisano J.J.;
RT "Vespulakinins: new carbohydrate-containing bradykinin derivatives.";
RL Biochemistry 15:61-64(1976).
RN [2]
RP SYNTHESIS.
RX MEDLINE=88057857; PubMed=3679673;
RA Rocchi R., Biondi L., Filira F., Scolari B.;
RT "Synthesis, conformation, and biological activity of the carbohydrate-
RT free vespulakinin 1.";

RL Int. J. Pept. Protein Res. 30:240-256(1987).
 CC -!- FUNCTION: Induces smooth muscle contraction.
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -!- SIMILARITY: Belongs to the bradykinin family.
 DR PIR; A61339; A61339.
 KW Bradykinin; Vasodilator; Glycoprotein.
 FT PEPTIDE 1 17 VESPULAKININ 1.
 FT PEPTIDE 3 17 VESPULAKININ 2.
 FT CARBOHYD 3 3 O-LINKED (GALNAC. . .).
 FT CARBOHYD 4 4 O-LINKED (GALNAC. . .).
 SQ SEQUENCE 17 AA; 1960 MW; 58B2CBA864122323 CRC64;

Query Match 20.4%; Score 20; DB 1; Length 17;
 Best Local Similarity 42.9%; Pred. No. 3.6e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 PDLQPFQ 15
 | ||:
 Db 11 PGFSPFR 17

RESULT 23

FIBA_LAMGL

ID FIBA_LAMGL STANDARD; PRT; 18 AA.
 AC P14454;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Lama glama (Llama), and
 OS Lama vicugna (Vicugna) (Vicugna vicugna).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 OX NCBI_TaxID=9844, 9843;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=L.glama;
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=L.vicugna;
 RA Moss G.A., Doolittle R.F.;
 RT "Amino acid sequence studies on artiodactyl fibrinopeptides.";
 RL Arch. Biochem. Biophys. 122:674-684(1967).
 CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 KW Blood coagulation; Plasma.

FT PEPTIDE 1 18 FIBRINOPEPTIDE A.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1834 MW; 2444487B8B7F4CC6 CRC64;

Query Match 20.4%; Score 20; DB 1; Length 18;
Best Local Similarity 60.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PDVEK 8
|| :|
Db 3 PDADK 7

RESULT 24

BPP3_BOTIN

ID BPP3_BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom."
RT J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 19.9%; Score 19.5; DB 1; Length 11;
Best Local Similarity 36.4%; Pred. No. 2.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 3 PPDVEKPDLP 13
|| :| :|
Db 4 PP---RPQIPP 11

RESULT 25

BPP4_BOTIN

ID BPP4_BOTIN STANDARD; PRT; 11 AA.
AC P30424;

DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom."
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; D37196; D37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 19.9%; Score 19.5; DB 1; Length 11;
 Best Local Similarity 36.4%; Pred. No. 2.7e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 3 PPDVEKPDLP 13
 || :| :|
 Db 4 PP--RPQIPP 11

RESULT 26

AL12_CARMA

ID AL12_CARMA STANDARD; PRT; 8 AA.
 AC P81815;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 12.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas."

RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 8 AA; 913 MW; 672879CDCB569AB7 CRC64;

Query Match 19.4%; Score 19; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 PDLQPF 14
||: |
Db 1 PDMYAF 6

RESULT 27

KNL3_BOMVA

ID KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens."
RL Submitted (JUL-2001) to Swiss-Prot.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the bradykinin family.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 19.4%; Score 19; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
| ||:
Db 3 PGFTPFR 9

RESULT 28

FARP_LOCFI

ID FARP_LOCFI STANDARD; PRT; 10 AA.
AC P38553;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SchistoFLRFamide (PDVDHFLRF-amide) (Cardioexcitatory neuropeptide).
OS Locusta migratoria (Migratory locust), and
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004, 7010;
RN [1]
RP SEQUENCE.
RC SPECIES=L.migratoria; TISSUE=Brain;
RX MEDLINE=93324430; PubMed=7687352;
RA Schoofs L., Holman G.M., Paemen L., Veelaert D., Amelinckx M.,
RA de Loof A.;
RT "Isolation, identification, and synthesis of PDVDHFLRFamide
RT (SchistoFLRFamide) in Locusta migratoria and its association with the
RT male accessory glands, the salivary glands, the heart, and the
RT oviduct.";
RL Peptides 14:409-421(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system;
RX MEDLINE=89246543; PubMed=2719702;
RA Robb S., Packman L.C., Evans P.D.;
RT "Isolation, primary structure and bioactivity of schistoflrf-amide, a
RT FMRF-amide-like neuropeptide from the locust, Schistocerca
RT gregaria.";
RL Biochem. Biophys. Res. Commun. 160:850-856(1989).
CC -!- FUNCTION: Muscle inhibiting agent. Involved in the neural control
CC of the visceral muscles of the heart, accessory glands and
CC oviduct. May be involved in the regulation of saliva secretion.
CC -!- TISSUE SPECIFICITY: Found in axons of the male accessory glands,
CC the salivary glands, the heart, and the oviduct.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; A32543; A32543.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 19.4%; Score 19; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PDVE 7
|||:
Db 1 PDVD 4

RESULT 29
BRK_MEGFL
ID BRK_MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascalikinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like

DE peptide ([Thr6]bradykinin)].
OS *Megascolia flavifrons* (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Scoliidae; Megascolia.
OX NCBI_TaxID=7437;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=87293024; PubMed=3617088;
RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
RT "Two kinins isolated from an extract of the venom reservoirs of the
RT solitary wasp *Megascolia flavifrons*."
RL Toxicon 25:527-535(1987).
RN [2]
RP SEQUENCE.
RC TISSUE=Venom;
RA Nakajima T., Piek T., Yashuara T., Mantel P.;
RT "Two kinins isolated from the venom of *Megascolia flavifrons*."
RL Toxicon 26:34-34(1988).
CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
CC activities (e.g. smooth muscle contraction).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- SIMILARITY: Belongs to the bradykinin family.
DR PIR; B26744; B26744.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.
DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11 MEGASCOLIAKININ.
FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 19.4%; Score 19; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PDLQPFQ 15
| |:
Db 3 PGFTPFR 9

RESULT 30

TKN_KASSE

ID TKN_KASSE STANDARD; PRT; 12 AA.
AC P08611;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin.
OS *Kassina senegalensis* (Senegal running frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8415;
RN [1]
RP SEQUENCE.

RC TISSUE=Skin secretion;
 RX MEDLINE=77246385; PubMed=891753;
 RA Anastasi A., Montecucchi P.C., Erspamer V., Visser J.;
 RT "Amino acid composition and sequence of kassinin, a tachykinin
 RT dodecapeptide from the skin of the African frog *Kassina*
 RT *senegalensis*.";
 RL Experientia 33:857-858(1977).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S07206; S07206.
 DR PDB; 1MYU; 16-OCT-02.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW 3D-structure.
 FT MOD_RES 12 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1336 MW; 91757AB89DD6DAB5 CRC64;

Query Match 19.4%; Score 19; DB 1; Length 12;
 Best Local Similarity 66.7%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 DVEKPD 10
 || ||
 Db 1 DVPKSD 6

RESULT 31

ODPA_CANFA

ID ODPA_CANFA STANDARD; PRT; 13 AA.
 AC P49823;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pyruvate dehydrogenase E1 component alpha subunit, somatic form
 DE (EC 1.2.4.1) (PDHE1-A type I) (Fragment).
 GN PDHA1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
 CC conversion of pyruvate to acetyl-CoA and CO(2). It contains

CC multiple copies of three enzymatic components: pyruvate
 .CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
 CC lipoamide dehydrogenase (E3).
 CC -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
 CC acetyldihydrolipoamide + CO(2).
 CC -!- COFACTOR: Thiamine pyrophosphate.
 CC -!- ENZYME REGULATION: E1 activity is regulated by phosphorylation
 CC (inactivation) and dephosphorylation (activation) of the alpha
 CC subunit (By similarity).
 CC -!- SUBUNIT: Tetramer of two alpha and two beta subunits.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 DR HSC-2DPAGE; P49823; DOG.
 KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
 KW Mitochondrion; Phosphorylation.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1510 MW; C97EEBF844085B19 CRC64;

Query Match 19.4%; Score 19; DB 1; Length 13;
 Best Local Similarity 42.9%; Pred. No. 3.8e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DVEKPD 11
 ::||
 Db 7 EIKKXDL 13

RESULT 32

SRY_URSAR

ID SRY_URSAR STANDARD; PRT; 17 AA.
 AC P36396;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Sex-determining region Y protein (Testis-determining factor)
 DE (Fragment).
 GN SRY OR TDF.
 OS Ursus arctos (Brown bear) (Grizzly bear).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 OX NCBI_TaxID=9644;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94214722; PubMed=8162229;
 RA Taberlet P., Mattock H., Dubois-Paganon C., Bouvet J.;
 RT "Sexing free-ranging brown bears Ursus arctos using hairs found in
 RT the field.";
 RL Mol. Ecol. 2:399-403(1993).
 CC -!- FUNCTION: Transcriptional activator which regulates a genetic
 CC switch in male development. It is responsible for initiating male
 CC sex determination. SRY HMG box recognizes DNA by partial
 CC intercalation in the minor groove.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Contains 1 HMG box domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; X74007; CAB37858.1; -.
KW DNA-binding; Nuclear protein; Transcription regulation; Activator;
KW Sexual differentiation.
FT NON_TER 1 1
FT DNA_BIND <1 >17 HMG BOX.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2070 MW; 7385F10073FABA4A CRC64;

Query Match 19.4%; Score 19; DB 1; Length 17;
Best Local Similarity 42.9%; Pred. No. 5e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 VEKPDLO 12
:| | :|
Db 9 LENPKMQ 15

RESULT 33

BPPB_AGKHA

ID BPPB_AGKHA STANDARD; PRT; 11 AA.
AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffii (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=242054;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 18.9%; Score 18.5; DB 1; Length 11;
Best Local Similarity 36.4%; Pred. No. 3.8e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 3 PPDVEKPDLOP 13

Db || :| : |
4 PP---RPKIPP 11

RESULT 34

LMT3_LOCMI

ID LMT3_LOCMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family."
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: Potent mediator of visceral muscle contractile activity
CC (myotropic activity).
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 18.4%; Score 18; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QPF 14
 |||
Db 3 QPF 5

RESULT 35

FAR6_PANRE

ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;

RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of RMRFamide-related
 RT peptides (FaRPs) from free-living nematode, *Panagrellus redivivus*."
 RL Submitted (JUL-2000) to Swiss-Prot.
 CC -!- FUNCTION: Myoactive.
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 18.4%; Score 18; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QPF 14
 |||
 Db 5 QPF 7

RESULT 36
 FARI_CALVO
 ID FARI_CALVO STANDARD; PRT; 12 AA.
 AC P41869;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliMIRFamide 1.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliFMRFamides) from the blowfly
 RT Calliphora vomitoria."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR PIR; E44787; E44787.
 KW Neuropeptide; Amidation.
 FT MOD_RES 12 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1390 MW; 2DDDB316914AB5A7 CRC64;

Query Match 18.4%; Score 18; DB 1; Length 12;
 Best Local Similarity 60.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQPPD 5
:| | |
Db 3 NQPSD 7

RESULT 37

HS9A_RAT

ID HS9A_RAT STANDARD; PRT; 12 AA.
AC P82995;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heat shock protein HSP 90-alpha (Fragment).
GN HSPCA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=21589773; PubMed=11732320;
RA Langer T., Fasold H.;
RT "Isolation and quantification of the heat shock protein 90 alpha and
RT beta isoforms from rat liver.";
RL Protoplasma 218:54-56(2001).
CC -!- FUNCTION: Molecular chaperone. Has ATPase activity (By
CC similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the heat shock protein 90 family.
DR InterPro; IPR001404; Hsp90.
DR PROSITE; PS00298; HSP90; PARTIAL.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD_RES 4 4 PHOSPHORYLATION (BY DS-DNA KINASE) (BY
FT SIMILARITY).
FT MOD_RES 6 6 PHOSPHORYLATION (BY DS-DNA KINASE) (BY
FT SIMILARITY).
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1432 MW; DE47C322CAB6C1B6 CRC64;

Query Match 18.4%; Score 18; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQP 3
| | |
Db 8 DQP 10

RESULT 38

EP65_HUMAN

ID EP65_HUMAN STANDARD; PRT; 13 AA.
AC P54963;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Erythrocyte 65 kDa protein (P65) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE.
 RX MEDLINE=90004678; PubMed=2507249;
 RA Hart G.W., Haltiwanger R.S., Holt G.D., Kelly W.G.;
 RT "Nucleoplasmic and cytoplasmic glycoproteins.";
 RL Ciba Found. Symp. 145:102-118(1989).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 DR GO; GO:0005737; C:cytoplasm; NAS.
 KW Glycoprotein.
 FT NON_TER 1 1
 FT CARBOHYD 2 2 O-LINKED (GLCNAC).
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1300 MW; D0B873344C61A776 CRC64;

Query Match 18.4%; Score 18; DB 1; Length 13;
 Best Local Similarity 45.5%; Pred. No. 5.4e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 1 DQPPDVEKPDL 11
 | | | : | |
 Db 1 DSP--VSQPSL 9

RESULT 39

PEDI_HYDAT

ID PEDI_HYDAT STANDARD; PRT; 13 AA.
 AC P80578;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Pedin.
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
 OC Hydridae; Hydra.
 OX NCBI_TaxID=6087;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96232307; PubMed=8674432;
 RA Hoffmeister S.A.H.;
 RT "Isolation and characterization of two new morphogenetically active
 RT peptides from Hydra vulgaris.";
 RL Development 122:1941-1948(1996).
 CC -!- FUNCTION: Morphogenetically active peptide. Active in foot
 CC development.
 KW Morphogen.
 SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 18.4%; Score 18; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PDVEK 8

Db ||| :
 9 PDVSE 13

RESULT 40

TY13_PHYRO

ID TY13_PHYRO STANDARD; PRT; 13 AA.
AC P04096;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-13.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylloidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RA Montecucchi P.C., Gozzini L., Erspamer V.;
RT "Primary structure determination of a tryptophan-containing
tridecapeptide from Phyllomedusa rohdei.";
RL Int. J. Pept. Protein Res. 27:175-182(1986).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; A05174; A05174.
KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 18.4%; Score 18; DB 1; Length 13;
Best Local Similarity 57.1%; Pred. No. 5.4e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 EKPDLP 13
 ||| |
Db 2 EKPYP 8

RESULT 41

MARI_ALTSP

ID MARI_ALTSP STANDARD; PRT; 14 AA.
AC P29399;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Marinostatin C-2 [Marinostatin C-1; Marinostatin D].
OS Alteromonas sp. (strain B-10-31).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Alteromonas.
OX NCBI_TaxID=29456;
RN [1]
RP SEQUENCE, AND ACTIVE SITE.
RX MEDLINE=92176155; PubMed=1794974;
RA Takano R., Imada C., Kamei K., Hara S.;
RT "The reactive site of marinostatin, a proteinase inhibitor from
marine Alteromonas sp. B-10-31.";

RL J. Biochem. 110:856-858(1991).
 CC -!- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
 CC NOT TRYPSIN.
 KW Serine protease inhibitor; Pyrrolidone carboxylic acid.
 FT PEPTIDE 1 14 MARINOSTATIN C-2.
 FT PEPTIDE 3 14 MARINOSTATIN C-1.
 FT PEPTIDE 4 14 MARINOSTATIN D.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 6 7 REACTIVE BOND.
 SQ SEQUENCE 14 AA; 1644 MW; 6E7CEEF92EF32E44 CRC64;

Query Match 18.4%; Score 18; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 QPF 14
 |||
 Db 1 QPF 3

RESULT 42

HS11_PINPS

ID HS11_PINPS STANDARD; PRT; 15 AA.
 AC P81083;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Probable class I heat shock protein (Water stress responsive protein
 DE 3) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=98418576; PubMed=9747804;
 RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
 RT "Water-deficit-responsive proteins in maritime pine."
 RL Plant Mol. Biol. 38:587-596(1998).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins."
 RL Electrophoresis 20:1098-1108(1999).
 RN [3]
 RP REVISION TO 1.
 RA Frigerio J.-M.;
 RL Submitted (SEP-2001) to Swiss-Prot.
 CC -!- SUBUNIT: Forms oligomeric structures (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- INDUCTION: By water stress.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein

CC (spot N144) is: 6.1, its MW is: 17 kDa.
 CC -!- SIMILARITY: Belongs to the small heat shock protein (HSP20)
 CC family.
 CC -!- SIMILARITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II
 CC WHICH ARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST
 CC AND CLASS IV WHICH IS IN THE ENDOMEMBRANE. THIS PROTEIN BELONGS
 CC TO CLASS I.
 DR InterPro; IPR002068; Hsp20.
 DR PROSITE; PS01031; HSP20; PARTIAL.
 KW Heat shock; Multigene family.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1847 MW; 87FC504C2EB1F2B7 CRC64;

Query Match 18.4%; Score 18; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFQ 15
 |||
 Db 12 PFQ 14

RESULT 43

PSAO_CUCSA

ID PSAO_CUCSA STANDARD; PRT; 15 AA.
 AC P42052;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem 1 reaction centre subunit 8 (Photosystem I 17.5 kDa
 DE protein) (Fragment).
 GN PSAM.
 OS Cucumis sativus (Cucumber).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
 OX NCBI_TaxID=3659;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cotyledon;
 RX MEDLINE=91355209; PubMed=1883835;
 RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
 RT "Characterization of genes that encode subunits of cucumber PS I
 RT complex by N-terminal sequencing."
 RL Biochim. Biophys. Acta 1059:141-148(1991).
 CC -!- FUNCTION: Essential for the activity of NADP photoreduction.
 DR PIR; E56819; E56819.
 KW Photosystem I; Photosynthesis; Chloroplast; Thylakoid; Membrane.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1714 MW; CA0BF5DAD403D9F4 CRC64;

Query Match 18.4%; Score 18; DB 1; Length 15;
 Best Local Similarity 57.1%; Pred. No. 6.2e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 DLQPFQV 16

Db | | | |
 4 DXPTFQV 10

RESULT 44

UC23_MAIZE

ID UC23_MAIZE STANDARD; PRT; 15 AA.
AC P80629;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 502)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.2, its MW is: 45.0 kDa.
DR Maize-2DPAGE; P80629; COLEOPTILE.
DR MaizeDB; 123955; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1557 MW; C974ED33E9A4EC28 CRC64;

Query Match 18.4%; Score 18; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DQPPD 5
 |:| |
Db 3 DKPGD 7

RESULT 45

LPK1_LOCF1

ID LPK1_LOCF1 STANDARD; PRT; 16 AA.
AC P20404;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 1 (LOM-PK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]

RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=91224474; PubMed=2026322;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
 RT myotropic peptide of Locusta migratoria.";
 RL Gen. Comp. Endocrinol. 81:97-104(1991).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR PIR; A49761; A49761.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 16 16 AMIDATION.
 SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;

Query Match 18.4%; Score 18; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QPF 14
 |||
 Db 10 QPF 12

RESULT 46

LCTN_LAMGL

ID LCTN_LAMGL STANDARD; PRT; 18 AA.
 AC P83315;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lactophorin (Whey protein) (Fragment).
 OS Lama glama (Llama).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 OX NCBI_TaxID=9844;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=20000588; PubMed=10531593;
 RA Kappeler S., Farah Z., Puhan Z.;
 RT "Alternative splicing of lactophorin mRNA from lactating mammary gland
 RT of the camel (Camelus dromedarius).";
 RL J. Dairy Sci. 82:1-10(1999).
 CC -!- SIMILARITY: Belongs to the PP3 / GLYCAM-1 family.
 DR GO; GO:0005576; C:extracellular; ISS.
 DR InterPro; IPR007906; GLYCAM-1.
 DR Pfam; PF05242; GLYCAM-1; 1.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2079 MW; CD59616E5B236AC6 CRC64;

Query Match 18.4%; Score 18; DB 1; Length 18;
 Best Local Similarity 30.8%; Pred. No. 7.5e+03;
 Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DQPPDVEKPDLP 13
:| | :| |
Db 6 NEPKDEIYMESQP 18

RESULT 47

BPP2_BOTJA

ID BPP2_BOTJA STANDARD; PRT; 10 AA.
AC P01022;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
DE inhibitor V-6-II).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01255; XAVI6B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 17.3%; Score 17; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 5.8e+03;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KPDLP 13
:| :|
Db 5 RPQIPP 10

RESULT 48

BPP8_BOTIN

ID BPP8_BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom."
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; H37196; H37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

 Query Match 17.3%; Score 17; DB 1; Length 10;
 Best Local Similarity 28.6%; Pred. No. 5.8e+03;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

 Qy 7 EKPDLQP 13
 : |:: |
 Db 4 QHPNIPP 10

RESULT 49
 EFG_CLOPA
 ID EFG_CLOPA STANDARD; PRT; 11 AA.
 AC P81350;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor G (EF-G) (CP 5) (Fragment).
 GN FUSA.
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flengsrud R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5."
 RL Electrophoresis 19:802-806(1998).
 CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
 CC the nascent protein chain from the A-site to the P-site of the
 CC ribosome.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
 CC EF-G/EF-2 subfamily.
 DR InterPro; IPR000795; EF_GTPbind.

DR PROSITE; PS00301; EFACITOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 17.3%; Score 17; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 KPDLQPFQ 15
| | : ||
Db 1 KYPLEKFQ 8

RESULT 50

RRPL_CHAV

ID RRPL_CHAV STANDARD; PRT; 11 AA.

AC P13179;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)

DE (L protein) (Fragment).

GN L.

OS Chandipura virus (strain I653514).

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Rhabdoviridae; Vesiculovirus.

OX NCBI_TaxID=11273;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89299473; PubMed=2741347;

RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,

RA Banerjee A.K.;

RT "Structure and expression of the glycoprotein gene of Chandipura
RT virus.";

RL Virology 171:285-290(1989).

CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.

CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).

CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
CC NUCLEOCAPSID (N) PROTEIN.

CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
CC PARAMYXOVIRUSES.

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DR EMBL; J04350; AAA42917.1; -.

KW Transferase; RNA-directed RNA polymerase.

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 17.3%; Score 17; DB 1; Length 11;

Best Local Similarity 75.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 DLQP 13

|||

Db 2 DLNP 5

Search completed: July 4, 2004, 04:41:27

Job time : 7.1791 secs